

161745

Schreiber, David

From: Foley, Shanon
Sent: Tuesday, August 02, 2005 8:04 AM
To: Schreiber, David
Subject: 10/808964

Hi David. Please search nt SEQ ID NO: 2 and its complement. Please also include an interference search.

Thank you.
Shanon

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 5, 2005, 01:25:13 ; Search time 5981 Seconds
(without alignments)

11283.723 Million cell updates/sec

Title: US-10-808-964A-2

Perfect score: 1773

Sequence: 1 ggtacctcgtgattgttc.....caaatcgcccttcgggtacc 1773

Scoring table: IDENTITY NUC

Gapop 10_0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_hic:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_gse1:*

9: gb_gse2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
c 1	56.6	3.2	1101	9	CNS00LT2
c 2	50.2	2.8	939	9	AL078714 Drosophila
c 3	48.6	2.7	870	4	AL059400 Drosophila
c 4	48.2	2.7	573	6	BG445569 GA_Ea002
c 5	47.6	2.7	1141	9	CD659610 EtESTef53
c 6	47.4	2.7	922	9	AG365778 Mus muscu
c 7	46.6	2.6	571	6	AL066784 Drosophila
c 8	46.6	2.6	857	5	CA741621 wialc.pko
c 9	46.6	2.6	909	9	BP162319 BP162319
c 10	46.4	2.6	560	6	AL076720 Drosophila
c 11	46	2.6	401	2	CA222795 SCEZFL403
c 12	45.2	2.5	460	7	AW255252 ML252 pep
c 13	45.2	2.5	540	7	CV144191 EST855400
c 14	45.2	2.5	621	7	CV140472 EST851681
c 15	45.2	2.5	649	7	CV137364 EST848573
c 16	45.2	2.5	670	7	CV138441 EST849650
c 17	45.2	2.5	703	7	CN784300 EST782391
c 18	45.2	2.5	724	7	CV140340 EST851549
c 19	45.2	2.5	727	7	CV142163 EST853372
c 20	45.2	2.5	729	7	CV137577 EST848786
c 21	45.2	2.5	744	7	CV146884 EST858093
c 22	45.2	2.5	757	7	CO413802 EST844187
c 23	45.2	2.5	767	7	CO409276 EST839661
c 24	45.2	2.5	768	7	CO410601 EST840986
					CV138839 EST850048

c 25	45.2	2.5	769	7	CO413933
c 26	45.2	2.5	788	7	CV136509
c 27	45.2	2.5	788	7	CV141605
c 28	45.2	2.5	790	7	CO414433
c 29	45.2	2.5	790	7	CV139795
c 30	45.2	2.5	791	7	CO411407
c 31	45.2	2.5	793	7	CV139994
c 32	45.2	2.5	793	7	CV141902
c 33	45.2	2.5	806	7	CV147450
c 34	45.2	2.5	813	7	CV143480
c 35	45.2	2.5	818	7	CV140283
c 36	45.2	2.5	820	7	CV141069
c 37	45.2	2.5	826	7	CO414543
c 38	45.2	2.5	827	7	CV147922
c 39	45.2	2.5	830	7	CN784715
c 40	45.2	2.5	830	7	CN785819
c 41	45.2	2.5	830	7	CO410131
c 42	45.2	2.5	837	7	CV141290
c 43	45.2	2.5	845	7	CO411008
c 44	45.2	2.5	852	7	CV149200
c 45	45.2	2.5	855	7	CV148673

ALIGNMENTS

RESULT 1
CNS00LT2/c 1101 bp DNA linear GSS 14-JUN-1999
LOCUS Drosophila melanogaster genome survey sequence TET3 end of BAC:
DEFINITION BACR48P19 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.

ACCESSION AL078714.1 GI:5102004
VERSION AL078714

KEYWORDS GSS.

SOURCE Drosophila melanogaster (fruit fly)

ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

REFERENCE 1 (bases 1 to 1101)

GENOSCOPE.

AUTHORS Direct Submission

TITLE Submitted (11-JUN-1999) Genoscope - Centre National de Sequencage :

JOURNAL BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

COMMENT - Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a

collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila

melanogaster genome using these BACs. For further information

please see <http://www.fruitfly.org> The BDGP Drosophila

melanogaster BAC library was prepared by Kazutoyo Osoegawa and

Aaron Mammoss in Pieter de Jong's laboratory in the Department of

Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,

NY. The library is named RPCI-98 and was constructed by partial

ECORI digestion of Drosophila DNA provided by the BDGP from the

isogenic strain Y2; cn bw sp, the same strain used for the BDGP's

p1 and EST libraries. A more detailed description of the library

and how to order individual BAC clones, the entire library, or

filters for hybridization from the BACPAC Resource Center can be

found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

Location/Qualifiers

1. 1101

/organism="Drosophila melanogaster"

/mol_type="genomic DNA"

/db_xref="taxon:7227"

/clone="BACR48P19"

/clone_lib="RPCI-98"

/note="end : TET3"

ORIGIN

Query Match 3.2%; Score 56.6; DB 9; Length 1101;

Best Local Similarity 21.6%; Pred. No. 0.00037;

	ORIGIN	/note="end : TET3"
	Query Match	2.8%; Score 50.2; DB 9; Length 939;
	Best Local Similarity	16.5%; Pred. No. 0.023;
	Matches 43; Conservative 120; Mismatches 98; Indels 0; Gaps 0;	
Qy	1341	CTTTGTAAACAAAGGCCACAGCCCTTAACCTATGACCATATGTAATACTCTCCTCCGCCCA 1400
Dd	318	CTTCTCYCCCATCMGCCCTCTCCCCCMCYATCCCTCMMMYHTTYMMCCCCECCMCM 377
Qy	1401	TACAATCCCCCAAACCCCTTCCTCACACTCCCCTTACTTCACACCCAAAACCTGTCTTGTA 1460
Dd	378	MMCHMTCCMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMTTTTMEHNTMTMMCMVTMT 437
Qy	1461	CTCCACCAATTGAATTACTTCCAACCAATAACAAAAAGGAATCAGCTTTGGGATGAGGCCTACA 1520
Dd	438	MMMMMMMMMTTMMTMMMMMMMMMMMMMMMMMMMMMTMMMMMMMTMMMMMMMMMHMT 497
Qy	1521	AACCTCTFAGAAAATGTGGACCACTAGCGCTCGGCCTTCGAAACAGTATATACGA 1580
Dd	498	MMMMHHMMMMHHHTTHMMMMMMMMMTMMTMMMMMMMMMMMTMMMMMMMMMMMHMM 557
Qy	1581	CCAGGACTACAAATATCCGTGT 1601
Dd	558	MMMMCMMMMMMTTWTCCGTCT 578

RESULT 3	870 bp	linear	EST 15-MAR-2001
BG445569/c			
LOCUS			
DEFINITION	870 bp	mrna	
	arboresum	7-10 dpa fiber library	Gossypium
	arboresum	cdna clone GA_Ea028F15f,	mrna sequence.
ACCESSION	BG445569		
VERSION	BG445569.1		
KEYWORDS	GI:13355137		
SOURCE			
	Gossypium arboresum		
ORGANISM	Gossypium arboresum		
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;		
	rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.		
REFERENCE	1 (bases 1 to 870)		
AUTHORS	Wing,R.A., Friesch,D., Yu,Y., Main,D., Rambo,T., Simmons,J.,		
	Henry,D., Wood,T.C., Leslie,A. and Wilkins,T.A.		
TITLE	An integrated analysis of the genetics, development, and evolution		
	of the cotton fiber		
JOURNAL	Unpublished (2000)		

```

COMMENT
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Seq primer: TAATACGACTCACTATAGGG
High quality sequence start: 6
High quality sequence stop: 659.
      Location/Qualifiers
          1..870
              /organism="Gossypium arboreum"
              /mol_type="mRNA"
              /strain="AKA"
              /cultivar="8400"
              /db_xref="taxon:29729"
              /clone="GA_Ea0028F15f"
              /tissue_type="Fibers isolated from bolls harvested 7-10
FEATURES
source

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dpaa"
/lab host="E. coli"
/clone_lib="Gossypium arboreum 7-10 dpa fiber library"
/note="vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"

ORIGIN
2.78; Score 48.6; DB 4; Length 870;
Query Match

```

Best Local Similarity 48.5%; Pred. No. 0.063; DB 6; Length 573;
 Matches 81; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

Qy 994 CACGCCGCCGAGCATCTTGGCCAGATCTTCGCCGCCGCCCGCTGGCTCGTCCACCCC 1053
 Db |||||
 567 CCCCCCCCNCNCC 508
 Qy 1054 CGCACCCGCTACGGTTGGAGAGGAAAATGGCATCTTTCAACACCGGCTCTCCGGCACC 1113
 Db |||||
 507 CCCCCCNCNCCNN 448
 Qy 1114 TTGGATATCTGTAAGCTACCACTAGACAGTCTAGAGCCCTCTCTGGGC 1160
 Db |||||
 447 TCCGATCACTTCAACGGCGTCCGCCACCATATCTCTCTTGGCGGC 401

RESULT 4
 CD659610 573 bp mRNA linear EST 19-JUN-2003
 LOCUS EtESTef53d09.y1 Eimeria tenella M5-6 Excised cDNA Eimeria tenella
 DEFINITION CDNA 5', mRNA sequence.
 ACCESSION CD659610
 VERSION CD659610.1 GI:31993425
 KEYWORDS EST.
 SOURCE Eimeria tenella
 ORGANISM Eimeria tenella
 Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Eimeriidae;
 Eimeria.

REFERENCE 1 (bases 1 to 573)
 AUTHORS Liberator,P., Diaz,C., Tang,K., Marra,M., Hillier,L., Kucaba,T.,
 Martin,J., Wylie,T., Underwood,K., Stepien,M., Theising,B.,
 Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Page,D.,
 Harvey,N., Schurk,R., Ritter,E., Kohn,S., Florence,N., Shin,T.,
 Jackson,Y., Cardenas,M., McCann,R., Waterston,R., Wilson,R. and
 Sibley,D.

TITLE WashU-Merck Eimeria tenella project
 JOURNAL Unpublished (1999)
 COMMENT Contact: David Sibley, Ph.D.
 WashU-Merck Eimeria tenella project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 Contact David Sibley (toxest@borcim.wustl.edu) for further
 information relating to organism, libraries, or clone availability.
 Seq primer: -40RP from Gibco.

FEATURES
 source
 1..573
 /organism="Eimeria tenella"
 /mol_type="mRNA"
 /db_xref="taxon:5802"
 /dev_stage="L518"
 /lab_host="E.Coli DH10B (GeneHog, Invitrogen, Inc)"
 /clone_lib="Eimeria tenella M5-6 Excised cDNA"
 /note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
 XhoI; Sporozoites were obtained from in vitro sporulated
 and excysted oocysts of E.tenella grown in chickens. cDNA
 was synthesized from poly mRNA using an oligo-dT primer
 containing a XhoI site. Following second strand synthesis,
 EcoRI adapters were ligated to the cDNA and products were
 size-selected on sephacryl S500. The cDNA were ligated to
 EcoRI/XhoI prepared lambda ZapII (Stratagene). The primary
 library was mass excised using ExAssist helper phage
 (Stratagene). The phagenids were precipitated with PBG
 8000, extracted with phenol/chloroform and electroporated
 into DH10B cells. The library may contain a small
 percentage of host or bacterial contaminants. Library
 materials provided by: Paul Liberator, Merck Research Labs
 Library constructed by: Paul Liberator, Merck Research
 Labs."

ORIGIN

Query Match 2.7%; Score 47.6; DB 9; Length 1141;
 Best Local Similarity 35.2%; Pred. No. 0.13; Indels 0; Gaps 0;
 Matches 95; Conservative 0; Mismatches 175;

Query Match 2.7%; Score 48.2; DB 6; Length 573;
 Best Local Similarity 52.8%; Pred. No. 0.074; Indels 0; Gaps 0;
 Matches 104; Conservative 0; Mismatches 93;

Qy 920 GTAATACTACAGCAGCGCACCTCTTCTCACTTTTATAGGATCAGGTATCAAGGAGCGTT 979
 Db |||||
 294 GAAATGGAGCAGCAGCTCCCTCATCTGCTTTTCAGCGTTACGTTTGTCTGCAGTTGCA 353
 Qy 980 ACCGACAGAGAAGACACCGCCCCCGAGCCATCTTGGCCAGATCTCCGCCCGCCCTT 1039
 Db |||||
 354 GCAGCAGCAGCAGCCACAGCGCGCTGCGCCCTGTCCCAACAGCAGCAGCAGCTCGCG 413
 Qy 1040 GGCTGCTCCACCCCGCCACCGCTACCGTTGGAGAGGAAAATGGCATCTTCAACACC 1099
 Db |||||
 414 GAAGGAGCGCCGCGCGCAGCAGCAACAGCAGCAGCAGCAGCAGCAGCAGCTTCTCTCCC 473
 Qy 1100 GCCTCTCCCGCACCTTC 1116
 Db |||||
 474 AGCTTCCCGCTGCTGC 490

RESULT 5
 AG365778/c 1141 bp DNA linear GSS 03-JUN-2004
 LOCUS AG365778 Mus musculus molossinus DNA, clone:MSMg01-168K18.TJ, genomic survey
 DEFINITION sequence.
 ACCESSION AG365778
 VERSION AG365778.1 GI:47976983
 KEYWORDS GSS.
 SOURCE Mus musculus molossinus
 ORGANISM Mus musculus molossinus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1
 AUTHORS Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
 TITLE BAC end Sequences of Library MSMg01
 JOURNAL Unpublished
 COMMENT 2 (bases 1 to 1141)
 Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
 Direct Submission
 Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
 and Chemical Research (RIKEN), Genomic Sciences Center (GSC), Japan
 1-7-22 Suehiro-chou, Tsukuba, Ibaraki, Japan, URL:http://hgp.gsc.riken.go.jp/,
 Tel:81-45-503-9111, Fax:81-45-503-9170
 Clones are derived from the mouse BAC library MSMg01. For BAC
 library availability, please contact Kuniya Abe (abe@rtc.riken.jp).
 Tsukuba Institute, Bio Resource Center,
 The Institute of Physical and Chemical Research (RIKEN) 3-1-1
 Koyadai, Tsukuba, 305-0074 Japan
 phone: 81-298-36-9189, fax: 81-298-36-9199
 e-mail: abe@rtc.riken.jp

PRIMERS
 Sequencing : TJ
 LIBRARY
 Vector : pBACE3.6
 R.Site 1 : EcoRI
 R.Site 2 : EcoRI.

FEATURES
 source
 1..1141
 /organism="Mus musculus molossinus"
 /mol_type="genomic DNA"
 /sub_species="molossinus"
 /db_xref="taxon:57486"
 /clone="MSMg01-168K18.TJ"
 /sex="male"
 /tissue_type="mixture of kidney and spleen"
 /clone_lib="MSMg01 Mouse Male BAC Library"

ORIGIN

Query Match 2.7%; Score 47.6; DB 9; Length 1141;
 Best Local Similarity 35.2%; Pred. No. 0.13; Indels 0; Gaps 0;
 Matches 95; Conservative 0; Mismatches 175;


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RESULT 10
CA222795/c
LOCUS
DEFINITION SCEZF14038H05.g FL4 Saccharum officinarum cDNA clone SCEZF14038H05
5', mRNA sequence.
ACCESSION CA222795
VERSION CA222795
KEYWORDS EST.
SOURCE Saccharum officinarum
ORGANISM Saccharum officinarum

REFERENCE
AUTHORS Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.
TITLE The libraries that made SUCEST
JOURNAL Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
COMMENT Centro de Arruda P
Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: parruda@unicamp.br
Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
http://www.bccccenter.fcav.unesp.br
Plate: 038 row: H column: 05
Seq primer: T7 Promoter Primer.
Location/Qualifiers
FEATURES
source
1..560
/organism="Saccharum officinarum"
/mol_type="mRNA"
/db_xref="taxon:4547"
/clone="SCEZF14038H05"
/lab_host="DH10B"
/clone_lib="PL4"
/note="Organ: Developed inflorescence and rachis
(20cm-long); Vector: pSport1; Site_1: SalI; Site_2: NotI;
An unidirectional cDNA library generated from (developed
inflorescence and rachis (20cm-long)). cDNA was prepared
from polyA+ mRNA using SuperScript Plasmid System Kit
(Invitrogen). The double-strand cDNAs were fractionated
in a sepharose Cl-2B 40cm-columns and fragments sizing
between 0.8 and 1.5 Kb were directionally cloned into the
vector. Details of each source of RNA and library
construction can be obtained at
http://sucest.lad.ic.unicamp.br/public"

ORIGIN
Query Match 2.6%; Score 46.4; DB 6; Length 560;
Best Local Similarity 58.0%; Pred. No. 0.24;
Matches 80; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

Qy 977 GTTACCGCAGAAAGACACCGCCCGCAGCATCTTGCGCAGATCTCCGCGCGCC 1036
Db 396 GGTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 337
Qy 1037 CCTGGCTGCTCCACCGCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1096
Db 336 GCTCCCTCCNCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 277
Qy 1097 CCGGCTCTCCGCGACCT 1114
Db 276 ACCACCTCCCGCGCACT 259

RESULT 11
AW255252
LOCUS
DEFINITION ML252 peppermint glandular trichome Mentha x piperita cDNA, mRNA
sequence.
ACCESSION AW255252
VERSION AW255252
KEYWORDS EST.
SOURCE Mentha x piperita (peppermint)
ORGANISM Mentha x piperita

REFERENCE
AUTHORS Lange,B.M., Wildung,M.R., Stauber,E.J., Sanchez,C., Pouchnik,D. and
Croteau,R.
TITLE Probing essential oil biosynthesis and secretion by functional
evaluation of expressed sequence tags from mint glandular trichomes
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (6), 2934-2939 (2000)
MEDLINE 20183992
PUBMED 10717007
COMMENT
Contact: Lange, B.M.
Institute of Biological Chemistry/Washington State University
Pullman, WA
Email: lange-m@mail.wsu.edu.
Location/Qualifiers
FEATURES
source
1..401
/organism="Mentha x piperita"
/mol_type="mRNA"
/cultivar="Black Mitcham"
/db_xref="taxon:34256"
/tissue_type="peltate glandular trichomes"
/cell_type="secretory"
/clone_lib="peppermint glandular trichome"
/note="Vector: lambda ZAPII"

ORIGIN
Query Match 2.6%; Score 46; DB 2; Length 401;
Best Local Similarity 55.7%; Pred. No. 0.28;
Matches 88; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

Qy 959 TGACGTATCCAAAGGAGCGTTACGCGAGAAGAGACACCGCCCGCAGCATCTTGCC 1018
Db 126 TGGCTTACTTACCTTCTCGCCACCAACCGCCATCGCCACCGCGCGGTGCTGCC 185
Qy 1019 AGATCTTCGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1078
Db 186 GCATCCATCTGACACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 245
Qy 1079 AAAATGCGATCTTCAACACCGCGCTCTCCGCGACCTTC 1116
Db 246 CCGCATCTCCGCGACACCTCCGCGTCCATCTCCATC 283

RESULT 12
CV144191/c
LOCUS
DEFINITION CV144191 Sequencing ESTs from loblolly pine embryos Pinus taeda
cDNA clone RP1D242 5' end, mRNA sequence.
ACCESSION CV144191
VERSION CV144191
KEYWORDS EST.
SOURCE Pinus taeda (loblolly pine)
ORGANISM Pinus taeda

REFERENCE
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiids; Coniferales; Pinaceae; Pinus; Pinus.
TITLE (bases 1 to 460)
JOURNAL Buell,C.R., Hsiao,J. and Cairney,J.
COMMENT Sequencing of ESTs from loblolly pine embryonic libraries
Unpublished (2004)
Contact: C. Robin Buell
Plant Genomics Group
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: rbuell@tigr.org
This clone is available through TIGR. Please contact pine@tigr.org
for further information

```


Email: rbuell@tigr.org
This clone is available through TIGR. Please contact pine@tigr.org
for further information
Seq primer: ATT TAG GTG ACA CTA TAG.

FEATURES

source
1. .621
/organism="Pinus taeda"
/mol_type="mRNA"
/cultivar="7-56 mother tree, open-pollinated tree from,
Lyons, Georgia, USA"
/db_xref="taxon:3352"
/clone="RPIAN51"
/lab_host="E.coli DH10B-Tona"
/clone_lib="Sequencing ESTs from loblolly pine embryos"
/note="Organ: Zygotic Embryo and Megagametophyte, Somatic
Embryo; Vector: pCMV-SPORT 6.1; Site 1: NotI; Site 2:
EcoRV; tissue: Whole megagametophytes isolated from pine
seeds, Whole embryos excised from these megagametophytes,
whole somatic embryos and suspensor tissue from tissue
culture, isolated from cell line A12. Pooled RNA from
zygotic embryos, megagametophytes, and somatic embryo was
used for library construction. Pine cones were harvested
weekly from open-pollinated 7-56 mother trees, collections
occurred from 7/01/02 until 10/15/02. Whole
megagametophytes were first isolated from pine seeds, and
whole embryos excised from these megagametophytes each was
flash frozen. Embryo development was assessed using the
system of Pullman et al (Pullman GS, Johnson S, Peter G,
Cairney J, Xu N. 2003. Loblolly pine somatic
embryogenesis: development of a maturation medium and
resulting embryo quality. Plant Cell Reports 21:747-758
http://link.springer.de/link/service/journals/00299/conte
nts/03/00586/). For photographs see Ciavatta et al 2001.
(Ciavatta VT, Morillon R, Pullman GS, Chrispeels M,
Cairney J. 2001. An aquaglyceroporin is abundantly
expressed early in the development of the suspensor and
the embryo proper of loblolly pine (Pinus taeda L.). Plant
Physiol. 127: 1556-1567
(http://www.plantphysiol.org/cgi/content/full/127/4/1556))
."

ORIGIN

Query Match 2.5%; Score 45.2; DB 7; Length 621;
Best Local Similarity 68.9%; Pred. No. 0.53;
Matches 62; Conservative 0; Mismatches 28; Indels 0; Gaps 0;
Qy 980 ACCGCGAAGAAGACACCGCCCGCAGCCATCTTGGCCAGATCTTCGCGCGCGCCCT 1039
Db 308 ACCGCGCGGTAAACACCGCGCGGTAGCCATCGCGCTCTACGCGCGCTCG 249
Qy 1040 GGCTCGTCCACCGCGCCACCGCTACCGTT 1069
Db 248 GCCTCGGCGCTCCACCGCGCTCCACTGTT 219

RESULT 15

CV138441/C
LOCUS CV138441 649 bp mRNA linear EST 07-SEP-2004
DEFINITION EST849650 Sequencing ESTs from loblolly pine embryos Pinus taeda
cDNA clone RPIB320 5' end, mRNA sequence.
CV138441
ACCESSION CV138441.1 GI:51900760
VERSION
KEYWORDS EST.
SOURCE Pinus taeda (loblolly pine)
ORGANISM Pinus taeda
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.
1 (bases 1 to 649)
Buell C.R., Hsiao J. and Cairney J.
Sequencing of ESTs from loblolly pine embryonic libraries
TITLE Unpublished (2004)
JOURNAL
COMMENT Contact: C. Robin Buell
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Email: rbuell@tigr.org
This clone is available through TIGR. Please contact pine@tigr.org
for further information
Seq primer: ATT TAG GTG ACA CTA TAG.

FEATURES

source
1. .649
/organism="Pinus taeda"
/mol_type="mRNA"
/cultivar="7-56 mother tree, open-pollinated tree from,
Lyons, Georgia, USA"
/db_xref="taxon:3352"
/clone="RPIB320"
/lab_host="E.coli DH10B-Tona"
/clone_lib="Sequencing ESTs from loblolly pine embryos"
/note="Organ: Zygotic Embryo and Megagametophyte, Somatic
Embryo; Vector: pCMV-SPORT 6.1; Site 1: NotI; Site 2:
EcoRV; tissue: Whole megagametophytes isolated from pine
seeds, Whole embryos excised from these megagametophytes,
whole somatic embryos and suspensor tissue from tissue
culture, isolated from cell line A12. Pooled RNA from
zygotic embryos, megagametophytes, and somatic embryos was
used for library construction. Pine cones were harvested
weekly from open-pollinated 7-56 mother trees, collections
occurred from 7/01/02 until 10/15/02. Whole
megagametophytes were first isolated from pine seeds, and
whole embryos excised from these megagametophytes each was
flash frozen. Embryo development was assessed using the
system of Pullman et al (Pullman GS, Johnson S, Peter G,
Cairney J, Xu N. 2003. Loblolly pine somatic
embryogenesis: development of a maturation medium and
resulting embryo quality. Plant Cell Reports 21:747-758
http://link.springer.de/link/service/journals/00299/conte
nts/03/00586/). For photographs see Ciavatta et al 2001.
(Ciavatta VT, Morillon R, Pullman GS, Chrispeels M,
Cairney J. 2001. An aquaglyceroporin is abundantly
expressed early in the development of the suspensor and
the embryo proper of loblolly pine (Pinus taeda L.). Plant
Physiol. 127: 1556-1567
(http://www.plantphysiol.org/cgi/content/full/127/4/1556))
."

ORIGIN

Query Match 2.5%; Score 45.2; DB 7; Length 649;
Best Local Similarity 68.9%; Pred. No. 0.53;
Matches 62; Conservative 0; Mismatches 28; Indels 0; Gaps 0;
Qy 980 ACCGCGAAGAAGACACCGCCCGCAGCCATCTTGGCCAGATCTTCGCGCGCGCCCT 1039
Db 326 ACCGCGCGGTAAACACCGCGCGGTAGCCATCGCGCTCTACGCGCGCTCG 267
Qy 1040 GGCTCGTCCACCGCGCCACCGCTACCGTT 1069
Db 266 GCCTCGGCGCTCCACCGCGCTCCACTGTT 237

Search completed: August 5, 2005, 06:31:56
Job time : 5981 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 4, 2005, 21:48:07 ; Search time 981 Seconds
(without alignments)
10698.982 Million cell updates/sec

Title: US-10-808-964A-2

Perfect score: 1773

Sequence: 1 ggtacctccgtgattgttc.....caaatggccttcgggtacc 1773

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_16Dec04.*

1: Geneseqn1980s.*

2: Geneseqn1990s.*

3: Geneseqn2000s.*

4: Geneseqn2001as.*

5: Geneseqn2001bs.*

6: Geneseqn2002as.*

7: Geneseqn2002bs.*

8: Geneseqn2003as.*

9: Geneseqn2003bs.*

10: Geneseqn2003cs.*

11: Geneseqn2003ds.*

12: Geneseqn2004as.*

13: Geneseqn2004bs.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1773	100.0	1773	9 AAL57177	AAL57177 Porcine c
c 2	1285.2	72.5	1768	6 ABX08205	ABX08205 PMWS-Porc
c 3	1278.8	72.1	1768	6 ABX08203	ABX08203 PMWS-Porc
c 4	1277.2	72.0	1768	6 ABX08207	ABX08207 CT-Porc
c 5	1274	71.9	1768	6 ABX08206	ABX08206 CT-Porc
c 6	1274	71.9	1768	6 ABX08204	ABX08204 PMWS-Porc
c 7	1270.8	71.7	1774	6 ABX08219	ABX08219 PMWS-Porc
c 8	1252	70.6	1762	6 ABX08202	ABX08202 PMWS-Porc
c 9	1218.2	68.7	1759	6 ABX08208	ABX08208 CT-Porc
c 10	1210.2	68.3	1759	6 ABX08220	ABX08220 PK-15-Por
c 11	1196.8	67.5	7460	4 AAH74867	AAH74867 Nucleotid
c 12	1196.8	67.5	7460	8 AAH94361	AAH94361 Rolling c
c 13	1195.8	67.4	5285	4 AAH74865	AAH74865 Nucleotid
c 14	1195.8	67.4	5285	8 AAH94355	AAH94355 Rolling c
c 15	1195.8	67.4	5650	4 AAH74866	AAH74866 Nucleotid
c 16	1195.8	67.4	5650	8 ABX94356	ABX94356 Rolling c
c 17	1059.8	59.8	1759	4 AAF75839	AAF75839 DNA fragm
c 18	1058.4	59.7	1768	9 AAL57176	AAL57176 Porcine c
c 19	1055.6	59.5	1759	2 AAX35013	AAX35013 Nucleotid
c 20	1053.2	59.4	3609	4 AAF28320	AAF28320 pJP107 do

c 21	981.2	55.3	1768	2 AAX35380	Aax35380 Nucleotid
c 22	981.2	55.3	1768	2 AAX35212	Aax35212 Nucleotid
c 23	981.2	55.3	1768	3 AAZ56871	Aaz56871 DNA seque
c 24	981.2	55.3	1768	4 AAF75837	Aaf75837 PCV DNA f
c 25	976.4	55.1	1768	2 AAX35381	Aax35381 Nucleotid
c 26	976.4	55.1	1768	2 AAX35213	Aax35213 Nucleotid
c 27	976.4	55.1	1768	3 AAZ56872	Aaz56872 DNA seque
c 28	976.4	55.1	1768	4 AAF75838	Aaf75838 PCV DNA f
c 29	967.2	54.6	1768	2 AAX35382	Aax35382 Nucleotid
c 30	967.2	54.6	1768	2 AAX35012	Aax35012 Genomic D
c 31	967.2	54.6	1768	2 AAX35214	Aax35214 Nucleotid
c 32	954	53.8	1767	2 AAX35378	Aax35378 Nucleotid
c 33	954	53.8	1767	2 AAX35210	Aax35210 Nucleotid
c 34	954	53.8	1767	3 AAZ56869	Aaz56869 DNA seque
c 35	954	53.8	1767	4 AAF75835	Aaf75835 PCV DNA f
c 36	952.4	53.7	1767	2 AAX35379	Aax35379 Nucleotid
c 37	952.4	53.7	1767	2 AAX35211	Aax35211 Nucleotid
c 38	952.4	53.7	1767	3 AAZ56870	Aaz56870 DNA seque
c 39	952.4	53.7	1767	4 AAF75836	Aaf75836 PCV DNA f
c 40	921	51.9	1759	2 AAX85593	Aax85593 Nucleotid
c 41	916.2	51.7	1759	2 AAX87992	Aax87992 Porcine c
c 42	742.2	41.9	1361	2 AAX83757	Aax83757 Porcine c
c 43	740.6	41.8	1786	2 AAX83755	Aax83755 Porcine c
c 44	738.4	41.6	1768	8 ABV72527	ABv72527 Nucleotid
c 45	725.6	40.9	1768	2 AAX83754	Aax83754 Porcine c

ALIGNMENTS

RESULT 1

AAL57177
ID AAL57177 standard; DNA; 1773 BP.

AC AAL57177;

XX

XX

DT 27-OCT-2003 (revised)

DT 09-OCT-2003 (first entry)

XX

DB Porcine circovirus type 1-2 chimeric DNA.

XX

XX

KW Porcine circovirus type 2; PCV1-2; PCV1; PMWS; weaning piglet; dyspnoea;

KW progressive weight loss; postweaning multisystemic wasting syndrome; db;

KW tachypnea; anaemia; diarrhoea; jaundice; virucide; vaccine; PCV2; gene;

KW viral infection; chimeric.

XX

OS Porcine circovirus type 1.

OS Porcine circovirus type 2.

OS Chimeric.

XX

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Key Location/Qualifiers

CDS 958..1659

FT /*tag= a

FT /product= "Porcine circovirus type 2 ORF2 capsid protein"

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PT New infectious chimeric nucleic acid molecule of porcine circovirus,
 PT useful for preventing and/or treating pigs against viral infection and/or
 PT postweaning multisystemic wasting syndrome.
 XX Claim 13; Fig 9; 85pp; English.

XX The invention relates to a novel infectious chimeric nucleic acid
 CC molecule of porcine circovirus (PCV1-2) which comprises a nucleic acid
 CC encoding an infectious, non-pathogenic PCV1 (porcine circovirus type 1)
 CC containing an immunogenic open 2) in place of a PCV1 ORF gene. Postweaning
 CC PCV2 (porcine circovirus type 2) is a complex disease of weaning
 CC multisystemic wasting syndrome (PMWS) is a complex disease of weaning
 CC piglets that is becoming increasingly more widespread. The condition
 CC poses a potentially serious economic threat to the swine industry, thus
 CC it has become important to develop a vaccine against PCV2, the primary
 CC causative agent of PMWS. PMWS mainly affects pigs between 5-18 weeks of
 CC age and clinical symptoms include progressive weight loss, dyspnoea,
 CC tachypnea, anaemia, diarrhoea and jaundice. The chimeric polynucleotide
 CC of the invention demonstrates virucide activity and may be utilised as a
 CC vaccine for PMWS. The methods and compositions of the present invention
 CC may be useful for the prevention and/or treatment of pigs against viral
 CC infection and/or PMWS. The current sequence is that of the PCV1-2
 CC chimeric DNA of the invention. (Updated on 27-Oct-2003 to standardise OS
 CC field)

XX SQ Sequence 1773 BP; 472 A; 511 C; 359 G; 431 T; 0 U; 0 Other;

Query Match 100.0%; Score 1773; DB 9; Length 1773;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1773; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTACCTCCGTGGATTCTCTCAGCAGTCTTCCAAATTTGCAAGTAGTAATCTCCGA 60
 DB 1 GGTACCTCCGTGGATTCTCTCAGCAGTCTTCCAAATTTGCAAGTAGTAATCTCCGA 60
 QY 61 TAGAGAGCTTCTACAGCTGGGACAGCAGTTGAGAGTACCATTCCTGGGGGGCTGATTG 120
 DB 61 TAGAGAGCTTCTACAGCTGGGACAGCAGTTGAGAGTACCATTCCTGGGGGGCTGATTG 120
 QY 121 CTGGTAATCAAAATACATGCGGGCCAAAAGGAAGACAGTACCCCTTTAGTCTCTACAGTC 180
 DB 121 CTGGTAATCAAAATACATGCGGGCCAAAAGGAAGACAGTACCCCTTTAGTCTCTACAGTC 180
 QY 181 AATGGATACCGGTTCACACAGTCTCAGTAGATCATCCCAAGTAAACAGCCATAAAATCA 240
 DB 181 AATGGATACCGGTTCACACAGTCTCAGTAGATCATCCCAAGTAAACAGCCATAAAATCA 240
 QY 241 TCCAAAACAACTTCTTCCATGATATCCATFCCCACTTATTTTCTAGGCTTC 300
 DB 241 TCCAAAACAACTTCTTCCATGATATCCATFCCCACTTATTTTCTAGGCTTC 300
 QY 301 CAGTAGGTGTCCTAGGTGAGCAAAATAGGGGGCCCACTGGCTCTTCCACACCGGGC 360
 DB 301 CAGTAGGTGTCCTAGGTGAGCAAAATAGGGGGCCCACTGGCTCTTCCACACCGGGC 360
 QY 361 GGGCCCACTAGCTGTACAGTGTCTTCAATCAGCTGTGCTCATCTTCCGCTCACT 420
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 QY 481 ACAGTACCAAGNCCCGTCTCCAAAGGGTACTCAGCAGTACAGCAGTGTGCTGGC 540
 DB 481 ACAGTACCAAGNCCCGTCTCCAAAGGGTACTCAGCAGTACAGCAGTGTGCTGGC 540
 QY 541 TTCCCTTGGTTCGCGAGCTCCACACTCGAATGATGTGGCTTCTTTACTGCAGTAT 600
 DB 541 TTCCCTTGGTTCGCGAGCTCCACACTCGAATGATGTGGCTTCTTTACTGCAGTAT 600
 QY 601 TCTTTATTCCTGCTGGTTCCTTTTCGATGTGGCAGCGGCAACCAATATAC 660
 DB 601 TCTTTATTCCTGCTGGTTCCTTTTCGATGTGGCAGCGGCAACCAATATAC 660

DB 601 TCTTTATTCCTGCTGGTTCCTTTTCGATGTGGCAGCGGCAACCAATATAC 660
 QY 661 CACTTCACCTTGTATAAAGTCTGCTTCTTAGCAAAATTCGCAAAACCCCTGAGGTGAGGA 720
 DB 661 CACTTCACCTTGTATAAAGTCTGCTTCTTAGCAAAATTCGCAAAACCCCTGAGGTGAGGA 720
 QY 721 GTTCTACCTCTTCCAAACCTTCTCGCCCAAAACAAATAATCAAAAAGGGAGATTGGA 780
 DB 721 GTTCTACCTCTTCCAAACCTTCTCGCCCAAAACAAATAATCAAAAAGGGAGATTGGA 780
 QY 781 AGCTCCGATATTTGTTTTTCTCTCTCGAAGGATTATTAAGGTGAACACCCACTC 840
 DB 781 AGCTCCGATATTTGTTTTTCTCTCTCGAAGGATTATTAAGGTGAACACCCACTC 840
 QY 841 TTATGSGTTCGCGCGCTTTTCTTCTGCTGGCAATTTCTACGCGTCCGAGGTGCTG 900
 DB 841 TTATGSGTTCGCGCGCTTTTCTTCTGCTGGCAATTTCTACGCGTCCGAGGTGCTG 900
 QY 901 CGCTGCCGAAGTGCCTGGTAATCTACAGCAGCGCATCTTTCTCACTTTTATAGGATG 960
 DB 901 CGCTGCCGAAGTGCCTGGTAATCTACAGCAGCGCATCTTTCTCACTTTTATAGGATG 960
 QY 961 ACGTATCCAAAGGAGGTTCACCGCAGAAAGACACCGCCCGCAGCCATCTTGGCCAG 1020
 DB 961 ACGTATCCAAAGGAGGTTCACCGCAGAAAGACACCGCCCGCAGCCATCTTGGCCAG 1020
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 DB 1021 ATCTCCGCGCGCTTCTGCTGCTCCACCCCGCCACCGCTACCGTTGGAGAAGAAA 1080
 QY 1081 AATGGCATCTTCAACACCGCTCTCCCGCACCTTCGGATATATCTGTCAAGGCTTACCA 1140
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 DB 1141 GTCAGAACGCTCTCTGGGGGGTGGATGATGAGATTTAATTTGACGACTTTGTTCCC 1200
 QY 1201 CCGGAGGGGGGACCAACAAATCTCTATACCTTTGAACTACTACAGAAATAAGAAAGTT 1260
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 DB 1321 GCTGTTATTTCTAGATGATTTGTAACAAAGGCGCACAGCCCTTAACCTATGACCCATAT 1380
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 DB 1441 ACACCCAAACCTGTTCTTGACTCCACCATTTGATTTCTTCCAAACCAATAACAAAGGAAT 1500
 QY 1501 CAGCTTTGAGTGGGTGACAACTCTAGAAATGTGACCAACCGCTAGGCTCGGCCTGGC 1560
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 DB 1561 TTCCAAAACAGTATATACGACACAGGACTACAAATATCCGTGTAAACCATGTATGTACAATTC 1620
 QY 1621 AGAGAAATTTAATCTTAAAGACCCCTTAAACCTTAAATGAATAAATAAATCAAT 1680
 DB 1621 AGAGAAATTTAATCTTAAAGACCCCTTAAACCTTAAATGAATAAATAAATCAAT 1680
 QY 1681 TACGATGTGATACAAAGGAGCTCAGTAATTTTATTTATATGGAAGGACAGGCT 1740
 DB 1681 TACGATGTGATACAAAGGAGCTCAGTAATTTTATTTATATGGAAGGACAGGCT 1740

QY 1741 GGGTCCACTGCTTCAAAATCGGCTTGGGTACC 1773
 DB 1741 GGGTCCACTGCTTCAAAATCGGCTTGGGTACC 1773

RESULT 2
 ID ABX08205/c
 XX ABX08205 standard; DNA; 1768 BP.
 AC ABX08205;
 XX 20-JAN-2003 (first entry)
 DT
 XX PMWS-Porcine circovirus (PCV) P4 genome.
 DE
 XX Porcine circovirus genome; PCV; vaccine; type I PCV strain;
 KW type II PCV strain; congenital tremor; pig; whole PCV vaccine;
 KW passive immunisation; ds.
 XX Porcine circovirus.
 OS
 XX WO200196377-A2.
 XX 20-DEC-2001.
 XX 15-JUN-2001; 2001WO-US019220.
 XX 15-JUN-2000; 2000US-0211710P.
 XX (PURD) PURDUE RES FOUND.
 XX Mittal SK, Stevenson GW, Choi J, Kiupel M, Kanitz CL;
 XX WPI; 2002-106466/14.
 XX New porcine circovirus (PCV) nucleic acids for use as a component of
 PT vaccines for treating or preventing congenital tremors in pigs.
 XX Claim 1; Page 84; 88pp; English.

The invention describes an isolated nucleic acid (I) from a porcine
 CC circovirus (PCV) where (I) comprises a sequence coding for a circovirus
 CC polypeptide. A vaccine comprising a PCV nucleic acid that encodes an
 CC immunogenic polypeptide of type I or type II PCV strain and a carrier, is
 CC useful for treating or preventing congenital tremors in a pig or its
 CC progeny (PCV type I is composed of PK-15-PCV and CT-PCV-P7; PCV type II
 CC is composed of PMWS-PCV-P1, PMWS-PCV-P2, -P3, -P4, and CT-PCV-P5, -P6).
 CC An isolated PCV strain (II) is useful for diagnosing a pathological cause
 CC of congenital tremors in a pig which involves determining whether the pig
 CC has been infected by PCV strain type I or type II. The determination of
 CC the infection is effected by detecting the presence of a PCV nucleic acid
 CC in a biological sample from the pig, by detecting hybridisation of an
 CC oligonucleotide. Optionally, the determination of infection is effected
 CC by detecting the presence of PCV polypeptide in a biological sample from
 CC the pig by detecting binding of an antibody that specifically binds a PCV
 CC polypeptide. Optionally, the determination of infection is effected by
 CC detecting the presence of antibodies directed against a PCV polypeptide
 CC in a biological sample of the pig. An expression vector (III) encoding a
 CC PCV polypeptide is useful as a vector vaccine against congenital tremors.
 CC (II) along with a suitable adjuvant is useful as a whole PCV vaccine,
 CC while the antigenic PCV polypeptides are used as components of subunit
 CC vaccines. Antibodies against PCV proteins are useful in passive
 CC immunisation strategies. This sequence represents a porcine circovirus
 CC genome

Sequence 1768 BP; 453 A; 358 C; 493 G; 464 T; 0 U; 0 Other;
 Query Match 72.5%; Score 1285.2; DB 6; Length 1768;
 Best Local Similarity 89.0%; Pred. No. 0;
 Matches 1462; Conservative 0; Mismatches 158; Indels 22; Gaps 6;

QY 135 ACTCGGGGCCAAAAAAGGAACAGTACCCCTTTAGTCTCTACAGTCAATGGATACCGGTC 194

1768 ACTCGGGGCCAAAAAAGGTACAGTTCCACCTTTTAGTCTCTACAGTCAATGGATACGATC 1709
 195 ACACAGTCTCAGTAGATCATCCCAAGGTAAACAGGCATAAAAATCATCAAAAACAAAC 254
 1708 ACACAGTCTCAGTAGATCATCCCAAGGCATAAAAATCATCAAAAACAAAC 1649
 255 TTCTTCTCCATGATATCATCCCAAGGTAAACAGGCATAAAAATCATCAAAAACAAAC 314
 1648 TTCTTCCATGGTAAACATCCCAAGGTAAACAGGCATAAAAATCATCAAAAACAAAC 1589
 315 AGGCTCAGCAAAATTAAGGGCCCACTGGCTCTTCCCAACAGGGGGGCCCACTATGAC 374
 1588 CGGGTCTGCAAAATTAAGCAGCCCAATTTGCTTTTACCAACAGGGGGGCCCACTATGAC 1529
 375 GTGTACAGAGTGTCTTCAATCAGCTGTCTTCCGCTCACTTCCCGCTCACTTTCAAAAGTTTCAAGC 434
 1528 GTGTACAGTGTCTTCAATCAGCTGTCTTCCGCTCACTTCCCGCTCACTTTCAAAAGTTTCAAGC 1469
 435 CAGCCCGCGAAATTTCTCATATAGTTACAGGAAATGTCTCGGCTACAGTCAACAAAGA 494
 1468 CAGCCCGCGAAATTTCTGACAAACGTTACAGGGTGTCTCTGCAACGGTCAACAGACT 1409
 495 CCGGCTCTCCAAAGGGTACTCAGCAGTAGACAGGTGTCTCGCTTCCCTGTGTTCCG 554
 1408 CCGGCTCTCCAAAGGGTACTCAGCAGTAGACAGGTGTCTCGCTTCCCTGTGTTCCG 1349
 555 CGGAGCTCCACACTCGATATAGTGGCTTCTTTACTGCAATATCTTTATTTCTGCTG 614
 1348 AGGAGCTCCACATTCATTAAGTAAGTTGCTTCTTTACTGCAATATCTTTATTTCTGCTG 1289
 615 GTGGTTCCTTTGCTTTCGATGTGGCAGCGGCAACCAAAATACCACTTCACTTGT 674
 1288 ATCAGTTCTTTGGCTTCTCGATGTGGCAGCGGCAACCAAAATACCACTTCACTTGT 1229
 675 AAAAGTCTGCTTCTTAGCAAAATTCGCAAAACCTTGGAGGTGAGAGTTCTACCCCTCTTC 734
 1228 AAAAGTGTGCTTCTTCAAAATTAGCAAAACCTTGGAGGTGAGAGTTCTGCTCTCTCTC 1169
 735 CAAACCTTCTCTCGCCACAAACAAATTAATCAAAAGGAGATTCGAAAGCTCCCGTATTTT 794
 1168 ATTACCTTCTCTCGCCACAAATTAATCAAAAGGAGATTCGAAAGCTCCCGTATTTT 1109
 795 GTTTTCTCTCTCGGAGGATTTAAGGGTGAACACCCACCTCTTTATGGGTTGGG 854
 1108 CTTGCGCTGCTTCTCGGAGGATTTAAGGGTGAACACCCACCTCTTTATGGGTTGGG 1049
 855 GCCTT-----TTCTGCTTGGCAATTT-----CACTGACGCTGCCGAGGTGCTGC 901
 1048 TCCTGCTTCTTCCATTTCTTGTGGGCAATGTTGCTGCTGAGGTGCTGCCGAGGTGCTGC 989
 902 CGCTGCGAAGTGGCTGGTAATACTACAGCAGCGCACTTCTTTTATAGGATGA 961
 988 CGCTGCGAAGTGGCTGGTAATACT--TACAGCGCACTTCTTTGTTTTCA-GCTATGA 932
 962 CGTATCCAAGAGGCGTTACCGCAAGAAGACACCCCGCCGAGCCATCTTGGCCAGA 1021
 931 CGTATCCAAGAGGCGTTACCGCAAGAAGACACCCCGCCGAGCCATCTTGGCCAGA 872
 1022 TCCTCGCGCGCGCTTGGCTGTGTCAACCCCGCCGAGGTGCTGAGGAGAGGAAAA 1081
 871 TCCTCGCGCGCGCTTGGCTGTGTCAACCCCGCCGAGGTGCTGAGGAGAGGAAAA 812
 1082 ATGSCATCTTCAACACCCGCTCTCCGCACTTTCGATATACGTCAAGGCTACCCAG 1141
 811 ATGGCATCTTCAACACCCGCTCTCCGCACTTTCGATATACGTCAAGGCTACCCAG 752
 1142 TCAGAACGCTCTCTGGGCGGTGACATGATGAGATTTAATATTGACGACTTTGTTCCTCC 1201
 751 TCAGAACGCTCTCTGGGCGGTGACATGATGAGATTTAATATTGACGACTTTGTTCCTCC 692
 1202 CGGAGGGGGGACCAACAAATCTCTATACCTTTGTAATCTACAGATTAAGAAGGTTA 1261

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Db 691 CGGAGGGGGAGCAACAAATCTCTATACCCCTTTGAATACTACAGAATAAGAAAAAGTTA 632
Qy 1262 AGGTTGAATTCGSCCTGCTCCCATCATCCAGGGTGATAGGGAGTGGGTCCACTG 1321
Db 631 AGGTTGAATTCGSCCTGCTCCCATCATCCAGGGTGATAGGGAGTGGGTCCACTG 572
Qy 1322 CTGTTATTCAGATGATACTTGTGTAAACAAAGGCCACAGCCCTTAACCTATGACCCATATG 1381
Db 571 CTGTTATTCAGATGATACTTGTGTAAACAAAGGCCCTCAGCCCTTAACCTATGACCCATATG 512
Qy 1382 TAACTACTCTCCGCGCATACAAATCCCAACCTCTCTACCACTCCCGTTACTTCA 1441
Db 511 TAACTACTCTCCGCGCATACAAATCCCAACCTCTCTACCACTCCCGTTACTTCA 452
Qy 1442 CACCCAACTGTTCTTGACTCCACCACTTCAATCTTCCCAACAAATAACAAAAGGAATC 1501
Db 451 CACCCAACTGTTCTTGACTCCCACTTATGATTACTTCCCAACAAATAACAAAAGGAATC 392
Qy 1502 AGCTTTGGATGAGGCTACAAACCTCTAGAAATGTGGACCACTAGGCTCGGCACCTGCGT 1561
Db 391 AGCTTTGGATGAGGATACAAACCTCTAGAAATGTAGACCACTAGGCTCGGCACCTGCGT 332
Qy 1562 TCGAACACGATATATACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 1621
Db 331 TCGAACACGATATATACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 272
Qy 1622 GAGAAATTAATCTTAAAGACCCCTTAAACCTTAAACCTTAAACCTTAAACCTTAAACCTT 1681
Db 271 GAGAAATTAATCTTAAAGACCCCTTAAACCTTAAACCTTAAACCTTAAACCTTAAACCTT 215
Qy 1682 ACAGTGTGATAACAAAAAGACTCAGTAATTTATTTTATATGGGAAAGGCGACAGGGT 1741
Db 214 ACAGTGTGAT--AAAAAGACTCAGTAATTTATTTTATATGGGAAATTCAGGGCATGGG 158
Qy 1742 GGTCCACTGCTTCAATCGGCC 1763
Db 157 GGGAAAGGGTGACCACTGGCC 136
```

RESULT 3

ABX08203/c

ID ABX08203 standard; DNA; 1768 BP.

XX AC

AC AC

XX AC

XX AC

XX AC

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XX Claim 1; Page 83; 88pb; English.

PS The invention describes an isolated nucleic acid (I) from a porcine
XX circovirus (PCV) where (I) comprises a sequence coding for a circovirus
CC polypeptide. A vaccine comprising a PCV nucleic acid that encodes an
CC immunogenic polypeptide of type I or type II PCV strain and a carrier, is
CC useful for treating or preventing congenital tremors in a pig or its
CC progeny (PCV type I is composed of PK-15-PCV and CT-PCV-P7; PCV type II
CC is composed of PMWS-PCV-P1, PMWS-PCV-P2, -P3, -P4, and CT-PCV-P5, -P6).
CC An isolated PCV strain (II) is useful for diagnosing a pathological cause
CC of congenital tremors in a pig which involves determining whether the pig
CC has been infected by PCV strain type I or type II. The determination of
CC the infection is effected by detecting the presence of a PCV nucleic acid
CC in a biological sample from the pig, by detecting hybridisation of an
CC oligonucleotide. Optionally, the determination of infection is effected
CC by detecting the presence of PCV polypeptide in a biological sample from
CC the pig by detecting binding of an antibody that specifically binds a PCV
CC polypeptide. Optionally, the determination of infection is effected by
CC detecting the presence of antibodies directed against a PCV polypeptide
CC in a biological sample of the pig. An expression vector (III) encoding a
CC PCV polypeptide is useful as a vector vaccine against congenital tremors.
CC (II) along with a suitable adjuvant is useful as a whole PCV vaccine,
CC while the antigenic PCV polypeptides are used as components of subunit
CC vaccines. Antibodies against PCV proteins are useful in passive
CC immunisation strategies. This sequence represents a porcine circovirus
CC genome

XX Sequence 1768 BP; 452 A; 360 C; 496 G; 460 T; 0 U; 0 Other;

Query Match 72.1%; Score 1278.8; DB 6; Length 1768;

Best Local Similarity 88.8%; Pred. No. 0;

Matches 1458; Conservative 0; Mismatches 162; Indels 22; Gaps 6;

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Qy 135 ACTGCGGGCCAAAAAGGACAGTACCCCTTTAGTCTCTACAGTCAATGGATACCGTTC 194
Db 1768 ACTGCGGGCCAAAAAGGACAGTACCCCTTTAGTCTCTACAGTCAATGGATACCGTTC 1709
Qy 195 ACACAGTCTCAGTAGATCATCCCAAGTACACGACCATAAAAATATCCAAAAACAAC 254
Db 1708 ACACAGTCTCAGTAGATCATCCCAAGTACACGACCATAAAAATATCCAAAAACAAC 1649
Qy 255 TTCTTCTCCATGATATCCATCCCAACCATTTATTTCTACAGTCTTCCAGTAGTGTCCCT 314
Db 1648 TTCTTCCATGATATCCATCCCAACCATTTATTTCTACAGTCTTCCAGTAGTGTGTTC 1589
Qy 315 AGGCTCAGCAAAATTAAGGCGCCACTGGCTCTCCACAGCGCGGGCGGCGCATATGAC 374
Db 1588 CGGCTCTGCAAAATTAAGGCGCCACTGGCTCTCCACAGCGCGGGCGGCGCATATGAC 1529
Qy 375 GTGTACAGCTGTCTTCCAAATCAGCTGTGTCATCTTCCCGCTCACATTTCAAAAGTTCCAG 434
Db 1528 GTGTACATGGTCTTCCAAATCAGCTGTGTCATCTTCCCGCTCACATTTCAAAAGTTCCAG 1469
Qy 435 CAGCCCGCGGAAATTTCTCATACTAGTTACAGGAAATCTCGGCTACAGTCCACCAAGA 494
Db 1468 CAGCCCGCGGAAATTTCTCATACTAGTTACAGGAAATCTCGGCTACAGTCCACCAAGT 1409
Qy 495 CCCGCTCTCCAAAGGGTACTCAGCAGTAGACAGGTGCTGGCTTCCCGCTGTTCCG 554
Db 1408 CCCGCTCTCCAAAGGGTACTCAGCAGTAGACAGGTGCTGGCTTCCCGCTGTTCCG 1349
Qy 555 CGGAGCTCCACACTCGATAGTATGTGGCTCTTTTACTGCAGTATTTCTTTTCTGCTG 614
Db 1348 AGGAGCTCCACATTCATAGTATGTTGCTCTTTTACTGCAATATTTCTTTTCTGCTG 1289
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Db 1288 ATCAGTTCCTTTTCTCGTCTTCTCGATGTGGCGGCGGACCAAAATACCACTTTCACCTT 1229
Qy 675 AAAAGTCTGCTTCTTAGCAAAATTCGCAAAATTCGAGGTGAGGTGTTCTGCTTCTCTC 734
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 1108 CTGCGCTCTCTCGGAGGATTATTCAGGAGTGAACACCCACCTTTTATGAGGTTGGG 1049
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 Db |||||
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 Qy CGCTGCGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 961
 Db |||||
 988 CGCTGCGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 932
 Qy GGTATCAAGAGGCTTACCGCAGAGAGACACCGCCCGCGAGCTGCTGCTGCTGCTGCTGCT 1021
 Db |||||
 931 CGTATCAAGAGGCTTACCGCAGAGAGACACCGCCCGCGAGCTGCTGCTGCTGCTGCTGCT 872
 Qy TCCTCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1081
 Db |||||
 871 TCCTCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 812
 Qy ATGGCATCTTCAACACCGCTCTCTCGCATCTTCTCGCATCTTCTCGCATCTTCTCGCATCT 1141
 Db |||||
 811 ATGGCATCTTCAACACCGCTCTCTCGCATCTTCTCGCATCTTCTCGCATCTTCTCGCATCT 752
 Qy TCAGAGCGCTCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1201
 Db |||||
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 Qy CGGAGGCGGCGACCAACAAATCTCTATACCTTTGAAATCTACAGATATAGAGAGGTTA 1261
 Db |||||
 691 CGGAGGCGGCGACCAACAAATCTCTATACCTTTGAAATCTACAGATATAGAGAGGTTA 632
 Qy AGGTGTAATCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1321
 Db |||||
 631 AGGTGTAATCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 572
 Qy CTGTTATCTAGATGATTAATCTTCTGATGATGATGATGATGATGATGATGATGATGATGAT 1381
 Db |||||
 571 CTGTTATCTAGATGATTAATCTTCTGATGATGATGATGATGATGATGATGATGATGATGAT 512
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 Db |||||
 511 TAAACTACTCTCTCGCGCATACAAATCTCTCTACCTTCTCTCTCTCTCTCTCTCTCTCTCTCT 452
 Qy CACCAAACTGTTCTTGAATCTTGAATCTTGAATCTTGAATCTTGAATCTTGAATCTTGAATCT 1501
 Db |||||
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 Qy AGCTTTGATGAGCTACAACTTGAATCTTGAATCTTGAATCTTGAATCTTGAATCTTGAATCT 1561
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 331 TCGAAAACAGTATATACGACGAGCTACATATATATATATATATATATATATATATATATATAT 272
 Qy GAGATTTAATCTTAAAGACCCCTTAAACCTTAAACCTTAAACCTTAAACCTTAAACCTTAAAC 1681
 Db |||||
 271 GAGATTTAATCTTAAAGACCCCTTAAACCTTAAACCTTAAACCTTAAACCTTAAACCTTAAAC 215
 Qy ACGATGATATACAAAGAGCTCAGTAATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 1741
 Db |||||
 214 ACGAAGTAT-----AAAAAGAGCTCAGTAATTTATTTATTTATTTATTTATTTATTTATTT 158
 Qy GGTCCATGCTTCAATTCGGCC 1763
 Db |||||
 157 GGGAAAGGCTGACGACTGGCC 136

RESULT 4
 ABX08207/c
 ID ABX08207 standard; DNA; 1768 BP.
 XX AC ABX08207;
 XX AC ABX08207;
 DT 20-JAN-2003 (first entry)
 XX CT-Porcine circovirus (PCV) P6 genome.
 DE Porcine circovirus genome; PCV; vaccine; type I PCV strain;
 KW type II PCV strain; congenital tremor; pig; whole PCV vaccine;
 KW passive immunisation; ds.
 XX Porcine circovirus.
 OS WO200196377-A2.
 XX PD 20-DEC-2001.
 XX PF 15-JUN-2001; 2001WO-US019220.
 XX PR 15-JUN-2000; 2000US-0211710P.
 XX PA (PURD) PURDUE RES FOUND.
 XX PI Mittal SK, Stevenson GW, Choi J, Kiupel M, Kanitz CL;
 XX WPI; 2002-106466/14.
 XX DR N-ESD; ABU02906, ABU02911, ABU02922, ABU02929, ABU02935, ABU02942,
 XX DR ABU02948, ABU02955, ABU02960, ABU02966, ABU02968.
 XX PT New porcine circovirus (PCV) nucleic acids for use as a component of
 XX PT vaccines for treating or preventing congenital tremors in pigs.
 XX PS Claim 1; Page 85-86; 88pp; English.
 XX CC The invention describes an isolated nucleic acid (I) from a porcine
 CC circovirus (PCV) where (I) comprises a sequence coding for a circovirus
 CC polypeptide. A vaccine comprising a PCV nucleic acid that encodes an
 CC immunogenic polypeptide of type I or type II PCV strain and a carrier, is
 CC useful for treating or preventing congenital tremors in a pig or its
 CC progeny (PCV type I is composed of PK-15-PCV and CT-PCV-P7; PCV type II
 CC is composed of PMWS-PCV-P1, PMWS-PCV-P2, -P3, -P4, and CT-PCV-P5, -P6).
 CC An isolated PCV strain (II) is useful for diagnosing a pathological cause
 CC of congenital tremors in a pig which involves determining whether the pig
 CC has been infected by PCV strain type I or type II. The determination of
 CC the infection is effected by detecting the presence of a PCV nucleic acid
 CC in a biological sample from the pig, by detecting hybridisation of an
 CC oligonucleotide. Optionally, the determination of infection is effected
 CC by detecting the presence of PCV polypeptide in a biological sample from
 CC the pig by detecting binding of an antibody that specifically binds a PCV
 CC polypeptide. Optionally, the determination of infection is effected by
 CC detecting the presence of antibodies directed against a PCV polypeptide
 CC in a biological sample of the pig. An expression vector (III) encoding a
 CC PCV polypeptide is useful as a vector vaccine against congenital tremors.
 CC (II) along with a suitable adjuvant is useful as a whole PCV vaccine,
 CC while the antigenic PCV polypeptides are used as components of subunit
 CC vaccines. Antibodies against PCV proteins are useful in passive
 CC immunisation strategies. This sequence represents a porcine circovirus
 CC genome
 XX SQ Sequence 1768 BP; 451 A; 362 C; 496 G; 459 T; 0 U; 0 Other;

Query Match 72.0%; Score 1277.2; DB 6; Length 1768;
 Best Local Similarity 88.7%; Pred. No. 0;
 Matches 1457; Conservative 0; Mismatches 163; Indels 22; Gaps 6;
 Qy 135 ACTGCGGGCCAAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 194
 Db 1768 ACTGCGGGCCAAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1709

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QY 195 ACACAGTCTCAGTAGATCATCCCAAGGTAAACGACCATATAAAATCATCCAAAACAAAC 254
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Db 1708 ACACAGTCTCAGTAGATCATCCCAAGGTAAACGACCATATAAAATCATCAATAACACAC 1649
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    |||
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    |||
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QY 962 CGTATCCAAAGAGCGTTTACGCAAGAGAGACACCGCCCGCGAGCCATCTTGGCCAGA 1021
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Db 871 TCCTCCGCGCGCCCTGCTGCTCCACCCCGCCACCGCTACCGTTGGAGAGGAAGA 812
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QY 1082 ATGGCATCTTCAACACCCGCTCTCCCGCACTTCCGATATACCTGTCAGGCTACCAACAG 1141
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Db 751 TCAGAACCGCTCTCTGGCGGTGACATGATGAGATTAATGAGCTTGAAGCTTTGTTCCCC 692
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QY 1202 CGGAGGGGGGCAACAAATACTCTATACCTTTGATTAATACTACAGATAAGAAAGTTA 1261
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Db 631 AGGTTGAATTTCTGCGCCTGCTCCCCCATCACCCAGGGTGATGGGGAGTGGGCTCCACTG 572
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Db 451 CACCCAAACCTGTTCTTGTACTCCACCATGATTAATTTCCAAACCAATAAACAAGGAATC 392
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    |||
Db 391 AGCTTTGGCTGAGGCTACAAACCTCTAGAAATGTGGACCACTAGGCTCGGCACCTGGT 332
    |||
QY 1562 TCGAAACAGTATATACGACCACTACAAATATCGGTGTAAACCATGTATGTACAATTCA 1621
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Db 331 TCGAAACAGTAAATACGACCACTACAAATATCGGTGTAAACCATGTATGTACAATTCA 272
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QY 1622 GAGAAATTAATCTTAAAGACCCCCCACTTAAACCCCTTAAATGAATATAAAACCAATT 1681
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Db 271 GAGAAATTAATCTTAAAGACCCCCCACTTAAACCCCTTAAATGAAT---AATAAAACCAATT 215
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QY 1682 ACCATGTGATAACAAAAAGACCTCAGTAAATTTTATATGGAAAGGCGACAGGGTG 1741
    |||
Db 214 ACAGAGTGAAT---AAAAAGACTCAGTAAATTTTATATGGAATTCAGGGCATGGGG 158
    |||
QY 1742 GGTCCACTGCTTCAAAATCGGCC 1763
    |||
Db 157 GGGAAAGGTGACAACTGGCC 136
    |||
```

RESULT 5

ABX08206/c
ID ABX08206 standard; DNA; 1768 BP.

XX AC ABX08206;

XX DT 20-JAN-2003 (first entry)

XX CT-Porcine circovirus (PCV) P5 genome.

XX Porcine circovirus genome; PCV; vaccine; type I PCV strain;
KW type II PCV strain; congenital tremor; pig; whole PCV vaccine;
KW passive immunisation; ds.

XX OS Porcine circovirus.

XX PN WO200196377-A2.

XX PD 20-DEC-2001.

XX PF 15-JUN-2001; 2001WO-US019220.

XX PR 15-JUN-2000; 2000US-0211710P.

XX (PURD) PURDUE RES FOUND.

XX PI Mittal SK, Stevenson GW, Choi J, Kiupel M, Kanitz CL;

XX WPI; 2002-106466/14.

DR N-PSDB; ABU02905, ABU02912, ABU02921, ABU02928, ABU02933, ABU02940,
DR ABU02947, ABU02954, ABU02961, ABU02964, ABU02972.

XX New porcine circovirus (PCV) nucleic acids for use as a component of
PT vaccines for treating or preventing congenital tremors in pigs.

XX PS Claim 1; Page 84-85; 88pp; English.

XX XX

CC The invention describes an isolated nucleic acid (I) from a porcine
 CC circovirus (PCV) where (I) comprises a sequence coding for a circovirus
 CC polyprotein. A vaccine comprising a PCV nucleic acid that encodes an
 CC immunogenic polypeptide of type I or type II PCV strain and a carrier, is
 CC useful for treating or preventing congenital tremors in a pig or its
 CC progeny (PCV type I is composed of PK-15-PCV and CT-PCV-P7; PCV type II
 CC is composed of PMS-PCV-P1, PMS-PCV-P2, -P3, -P4, and CT-PCV-P5, -P6).
 CC An isolated PCV strain (II) is useful for diagnosing a pathological cause
 CC of congenital tremors in a pig which involves determining whether the pig
 CC has been infected by PCV strain type I or type II. The determination of
 CC the infection is effected by detecting the presence of a PCV nucleic acid
 CC in a biological sample from the pig, by detecting hybridisation of an
 CC oligonucleotide. Optionally, the determination of infection is effected
 CC by detecting the presence of PCV polypeptide in a biological sample from
 CC the pig by detecting binding of an antibody that specifically binds a PCV
 CC polypeptide. Optionally, the determination of infection is effected by
 CC detecting the presence of antibodies directed against a PCV polypeptide
 CC in a biological sample of the pig. An expression vector (III) encoding a
 CC PCV polypeptide is useful as a vector vaccine against congenital tremors.
 CC (II) along with a suitable adjuvant is useful as a whole PCV vaccine,
 CC while the antigenic PCV polypeptides are used as components of subunit
 CC vaccines. Antibodies against PCV proteins are useful in passive
 CC immunisation strategies. This sequence represents a porcine circovirus
 CC genome
 CC
 CC

XX SQ Sequence 1768 BP; 451 A; 361 C; 497 G; 459 T; 0 U; 0 Other;

Query Match 71.9%; Score 1274; DB 6; Length 1768;

Best Local Similarity 88.6%; Pred. No. 0;
 Matches 1455; Conservative 0; Mismatches 165; Indels 22; Gaps 6;

Qy 135 ACTGGGCGCAAAAGGAACAGTACCCCTTTAGTCTCTACAGTCAATGGATCCGGTC 194
 Db 1768 ACTGGGCGCAAAAGGAAGTACAGTTCCACCTTTAGTCTCTACAGTCAATGGATCCGATC 1709
 Qy 195 ACACAGTCTCAGTAGATCATCCCAAGGTAAACAGCCATAAATCATCAAAACACAC 254
 Db 1708 ACACAGTCTCAGTAGATCATCCCAAGGTAAACAGCCATAAATCATCAAAACACAC 1649
 Qy 255 TTCTTCTCATGATATCCATCCACCACTTATTTCTAGCTTCCAGTAGGTGTCCT 314
 Db 1648 TTCTTCTCATGATATCCATCCACCACTTATTTCTAGCTTCCAGTAGGTGTCCT 1589
 Qy 315 AGGCTCAGCAAAATTAACGGGCGCACTGGCTCTTCCACAAACGGGCGGCGCCACTATGAC 374
 Db 1588 CGGCTCTGCAAAATTAACGAGCCCAATTTGCTTTTACCAACAGGTGCGCCCAACATGAC 1529
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 Db 1528 GTGTACATGTGCTTCTTCCAAATCAGCTGTGATCTTCCGGCTCAGTTTCAAAAGTTGAGC 1469
 Qy 435 CAGCCCGGGAAATTTCTCAGATGTTTACAGGAACTGCTCGGTACAGTCAACCAAGA 494
 Db 1468 CAGCCCGGGAAATTTCTCAGATGTTTACAGGAACTGCTCGGTACAGTCAACCAAGT 1409
 Qy 495 CCGGCTCTCCAAAGGGTACTCACAGCAGTAGACAGGTGCGTCTCCCTGGTTCCG 554
 Db 1408 CCGGCTCTCCAAAGGGTACTCACAGCAGTAGACAGGTGCGTCTCCCTGGTTCCGATCG 1349
 Qy 555 CGGAGCTCCACATCGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 614
 Db 1348 AGGAGCTCCACATCAATTAAGTAAGTTGCTTCTTACTGCAATATTTCTTATTTCTGCTG 1289
 Qy 615 GTCCGTTCTTCTGCTTCTGATGTCAGCGGCGCACCAAAATACCACTTCACTTGT 674
 Db 1288 ATCAGTCTTCTTGGCTTCTGATGTCAGCGGCGCACCAAAATACCACTTCACTTAT 1229
 Qy 675 AAAAGTCTGCTTCTTAGCAAAATTCGCAAAACCCCTGGAGGTGAGGAGTTCTACCCCTTTC 734
 Db 1228 GAAAGTTTGTCTTCTTCAAAATTAGCGAAACCCCTGGAGGTGAGGAGTTCTGCTCTTCTC 1169
 Qy 735 CAAACCTTCTCGGCAACAAATTAATCAAAAGGGAGATTTGAGAGTCCCGTATTTT 794

Db 1168 ATTACCTCTCTCGGCAACAAATAAATAAATAGGAGATTTGGAGCTCCCGTATTTT 1109
 Qy 795 GTTTTCTCTCTCGGAAAGGATTAATAAGGTTGAACACCCACCTCTCTTATGGGGTTGGG 854
 Db 1108 CTGGCTCGTCTTCGGAAGGATTAATCAGCGTGAACACCCACCTTTTATGTGGTTGGG 1049
 Qy 855 GCGGCTT-----TTCTTGTCTGGCATTTT-----CACTGACGCTGCGAGGTGCTGC 901
 Db 1048 TCCGCTTCTTCCATTTCTTCTTGTGGGCAATGTTGCTGTGAGGTCTGCGGAGGTGCTGC 989
 Qy 902 CGCTGCCGAAGTGGCTGCTGTAATACTACAGCAGGCGCACTTCTTTCACCTTTTATAGATGA 961
 Db 998 CGCTGCCGAAGTGGCTGCTGTAATACT--TACAGCGCACTTCTTCTGTTTTCTA-GCTATGA 932
 Qy 962 CGTATCCAAGGAGGGCTTTACCGCAGAGAAAGACACCGCCCGCAGCCACTCTTGGCCAGA 1021
 Db 931 CGTATCCAAGGAGGGCTTTACCGCAGAGAAAGACACCGCCCGCAGCCACTCTTGGCCAGA 872
 Qy 1022 TCCTCCGCGCGGCTCTGGCTCGTCTCACCCTCGGCGCACCGCTACCGTTGGAGAGGAAAA 1081
 Db 871 TCCTCCGCGCGGCTCTGGCTCGTCTCACCCTCGGCGCACCGCTACCGTTGGAGAGGAAAA 812
 Qy 1082 ATGCGCATCTTCAACACACCGGCTCTCCGCACTTTCGGATATATCTCAAGGCTACACAG 1141
 Db 811 ATGCGCATCTTCAACACACCGGCTCTCCGCACTTTCGGATATATCTCAAGGCTACACAG 752
 Qy 1142 TCAGAAAGCCCTCTCTGGGCGGTGACATGATGAGATTTAATATTGACGACTTTTGTTCGCC 1201
 Db 751 TCAGAAAGCCCTCTCTGGGCGGTGACATGATGAGATTTAAGCTTGGACGACTTTTGTTCGCC 692
 Qy 1202 CGGAGGAGGGGACCAAAATCTCTATACCTTTTGAATATCTACAGAAATAGAAAGTTA 1261
 Db 691 CGGAGGAGGGGACCAAAATCTCTATACCTTTTGAATATCTACAGAAATAGAAAGTTA 632
 Qy 1262 AGTTTGAATCTGCGGCTCTCCGCTACCCAGGTGATAGGGAGTGGGCTCCACTG 1321
 Db 631 AGTTTGAATCTGCGGCTCTCCGCTACCCAGGTGATAGGGAGTGGGCTCCACTG 572
 Qy 1322 CTGTTATTTAGATGATAACTTTGTAAACAAAGGGCCACAGCCCTAACCTATGACCCATATG 1381
 Db 571 CTGTTATTTAGATGATAACTTTGTAAACAAAGGGCCATGCGCTAACCTATGACCCATATG 512
 Qy 1382 TAAACTACTCTCCGCGCATCAATTCGCCCAACCCCTTCTCTACCACTCCCGTTACTTCA 1441
 Db 511 TAAACTACTCTCCGCGCATCAATTCGCCCAACCCCTTCTCTACCACTCCCGTTACTTCA 452
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 Db 451 CACCAACCTGTTCTTGACTCCCACTTGATTTACTTCCAAACCAATTAACAAAGGAATC 392
 Qy 1502 AGCTTTGGATGAGGCTTACAAACCTCTAGAAATGTGGACACAGTGGGCTCGGCACTGGGT 1561
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 Db 214 ACAGTGTGAT---AAAAAGACTCAGTAATTTATTTTATATGGGAAAGGCGACAGGGTG 158
 Qy 1742 GGTCCACTGCTTCAAAATCGGCC 1763
 Db 157 GGGAAAGGGTGACGAACTGGCC 136

RESULT 6
 ABX08204/c

ID ABX08204 standard; DNA; 1768 BP.
 AC ABX08204;
 XX
 XX 20-JAN-2003 (first entry)
 DT
 XX PMS-Porcine circovirus (PCV) P3 genome.
 XX
 XX Porcine circovirus genome; PCV; vaccine; type I PCV strain;
 KW type II PCV strain; congenital tremor; pig; whole PCV vaccine;
 KW passive immunisation; ds.
 XX
 XX Porcine circovirus.
 OS
 XX W0200196377-A2.
 XX
 XX 20-DEC-2001.
 PD
 XX
 XX 15-JUN-2001; 2001WO-US019220.
 PF
 XX
 XX 15-JUN-2000; 2000US-0211710P.
 PR
 XX (PURD) PURDUE RES FOUND.
 XX
 XX Mittal SK, Stevenson GW, Choi J, Kiupel M, Kanitz CL;
 PI
 XX WPI; 2002-106466/14.
 DR
 DR N-PSDB; ABU02904, ABU02910, ABU02919, ABU02926, ABU02932, ABU02939,
 DR ABU02945, ABU02952, ABU02958, ABU02963, ABU02970.
 XX
 XX New porcine circovirus (PCV) nucleic acids for use as a component of
 PT vaccines for treating or preventing congenital tremors in pigs.
 XX
 XX Claim 1; Page 83-84; 88pp; English.
 PS
 XX
 XX The invention describes an isolated nucleic acid (I) from a porcine
 CC circovirus (PCV) where (I) comprises a sequence coding for a circovirus
 CC polypeptide. A vaccine comprising a PCV nucleic acid that encodes an
 CC immunogenic polypeptide of type I or type II PCV strain and a carrier, is
 CC useful for treating or preventing congenital tremors in a pig or its
 CC progeny (PCV type I is composed of PK-15-PCV and CT-PCV-P7; PCV type II
 CC is composed of PMS-PCV-P1, PMS-PCV-P2, -P3, -P4, and CT-PCV-P5, -P6).
 CC An isolated PCV strain (II) is useful for diagnosing a pathological cause
 CC of congenital tremors in a pig which involves determining whether the pig
 CC has been infected by PCV strain type I or type II. The determination of
 CC the infection is effected by detecting the presence of a PCV nucleic acid
 CC in a biological sample from the pig, by detecting hybridisation of an
 CC oligonucleotide. Optionally, the determination of infection is effected
 CC by detecting the presence of PCV polypeptide in a biological sample from
 CC the pig by detecting binding of an antibody that specifically binds a PCV
 CC polypeptide. Optionally, the determination of infection is effected by
 CC detecting the presence of antibodies directed against a PCV polypeptide
 CC in a biological sample of the pig. An expression vector (III) encoding a
 CC PCV polypeptide is useful as a vector vaccine against congenital tremors.
 CC (II) along with a suitable adjuvant is useful as a whole PCV vaccine,
 CC while the antigenic PCV polypeptides are used as components of subunit
 CC vaccines. Antibodies against PCV proteins are useful in passive
 CC immunisation strategies. This sequence represents a porcine circovirus
 CC genome
 XX
 SQ Sequence 1768 BP; 451 A; 361 C; 497 G; 459 T; 0 U; 0 Other;
 Query Match 71.98; Score 1274; DB 6; Length 1768;
 Best Local Similarity 88.68; Pred. No. 0;
 Matches 1455; Conservative 0; Mismatches 165; Indels 22; Gaps 6;
 135 ACTGCGGGCCAAAAGGACAGTACCCCTTTAGTCTCTACAGTCAATGATACCGGTC 194
 1768 ACTGCGGGCCAAAAGGACAGTACCCCTTTAGTCTCTACAGTCAATGATACCGGTC 1709
 195 ACACAGTCTCAGTAGATCATCCCAAGGTAAACGCCATAAAATCATCCAAAACAAC 254
 1708 ACACAGTCTCAGTAGATCATCCCAAGGTAAACGCCATAAAAGTCATCAATAACAC 1649

QY 255 TTCTTCTCATGATATCCATCCACACCTTTAATTTCTACTAGGCTTCCAGTAGGTGTCCT 314
 DB 1648 TTCTTACCATGGTAACCATCCACCACTTGTTTCTAGTGGTTTCCAGTATGGGTTTC 1589
 QY 315 AGGCTCAGCAAAATTAAGGCCCCACTGGCTCTTCCCAACAAACGGGGGGCCACTATGAC 374
 DB 1588 CGGGTCTGCAAAATTAAGCAGCCCAATTTGCTTTTACCACACAGGTTGGCCCAATGAC 1529
 QY 375 GTGTACAGCTGTCTTCCAAATCAGCTGTGCTATCTTCCCGCTCAGTTTCAAAAGTTTCAGC 434
 DB 1528 GTGTACATTTGGTCTTCCAAATCAGCTTCTGCAATTTTCCCGCTCAGTTTCAAAAGTTTCAGC 1469
 QY 435 CAGCCCGCGGAAATTTCTCACATACGTTACAGGAAACTGCTCGGCTACAGTACCAAGA 494
 DB 1468 CAGCCCGCGGAAATTTCTGACAAACGTTACAGGGTGTCTCTGCAACGGTCAACGACT 1409
 QY 495 CCGGCTCTCAAAAGGGTACTCAGCAGTAGACAGTCTGCTGCTGCTGCTGCTGCTGCTGCTG 554
 DB 1408 CCGGCTCTCAAAAGGGTACTCAGCAGTAGACAGTCTGCTGCTGCTGCTGCTGCTGCTGCTG 1349
 QY 555 CCGGCTCTCAAAAGGGTACTCAGCAGTAGACAGTCTGCTGCTGCTGCTGCTGCTGCTGCTG 614
 DB 1348 AGGAGCTCCACATTTCAATAAGTAAAGTTGCTTTCTTACTGCAATATTTCTTATTTCTGCTG 1289
 QY 615 GTGCTTCTCTCGCTTCTCGATGTGGCAGCGGCAACCAAAATACCAATACCACTTTCACCTTGT 674
 DB 1288 ATCAGTCTCTTGGCTTCTCGATGTGGCAGCGGCAACCAAAATACCAATACCACTTTCACCTTGT 1229
 QY 675 AAAAGTCTGCTTCTTAGCAAAATTCGCAAAACCCCTGGAGGTGAGGAGTCTTACCTCTTC 734
 DB 1228 GAAAGTTGCTTCTTCAAAATTTAGCAAAACCCCTGGAGGTGAGGAGTCTTACCTCTTC 1169
 QY 735 CAACCTTCTCTCGCAACCAAAATTAATCAAAAGGAGATTTGGAGCTCCCGTATTTT 794
 DB 1168 ATTACCTCTCTCGCAACCAAAATTAATCAAAAGGAGATTTGGAGCTCCCGTATTTT 1109
 QY 795 GTTTTCTCTCTCGCAAGGATTTAATAGGGTGAAACACCCACTCTTATGGGGTTCGGG 854
 DB 1108 CTTGGCTGCTCTTGGAGGATTTATCAGCTGTAACACCACTTTTATGTGGTGGG 1049
 QY 855 GCGGCTT-----TTCTTGTCTGGCATTTT-----CACTGAGCTGCGGAGTGTGTC 901
 DB 1048 TCGGCTTCTTCCATTTCTTGTGCGCATGTTGCTGCTGAGGTGCTGCGGAGTGTGTC 989
 QY 902 CGCTGCGAGTGGCTGTAATTAATACAGCGGCACTTTCTTCTTCTTATAGGATGA 961
 DB 988 CGTGGCGAAGTGGCTGGTAATTAATTAAGGCACTTTCTTCTGTTTTCA-GCTATGA 932
 QY 962 CGTATCAAGGAGCGTTACCGCAGAAAGACACACCGCCCGCAGCCATCTTGGCCAGA 1021
 DB 931 CGTATCAAGGAGCGTTACCGCAGAAAGACACACCGCCCGCAGCCATCTTGGCCAGA 872
 QY 1022 TCCTCGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1081
 DB 871 TCCTCGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 812
 QY 1082 ATGGCATCTTCAACACCGGCTCTCCGCACTTCGGATATCTGTCAAGGTACCAACAG 1141
 DB 811 ATGGCATCTTCAACACCGGCTCTCCGCACTTCGGATATCTGTCAAGGTACCAACAG 752
 QY 1142 TCAGAACGCGCTCTCTGGCGGTGGACATGATGAGATTTAATAATTGACGACTTTTGTCCCC 1201
 DB 751 TCAGAACGCGCTCTCTGGCGGTGGACATGATGAGATTTAAGCTTGGACACTTTTGTCCCC 692
 QY 1202 CGGAGGGGGGACCAACAAATCTCTATACCTTTGTAATCTACAGATTAAGAAGTTA 1261
 DB 691 CGGAGGGGGGACCAACAAATCTCTATACCTTTGTAATCTACAGATTAAGAAGTTA 632
 QY 1262 AGGTTGAATTTCTGCGCTGCTCCCCCATCAACAGGCTGATAGGGAGTGGGCTCCACTG 1321
 DB 631 AGGTTGAATTTCTGCGCTGCTCCCCCATCAACAGGCTGATAGGGAGTGGGCTCCACTG 572

QY 1322 CTGTTATTCTAGATGATTAACCTTTGTAACAAAGGCCACAGCCCTACCTATGACCCATATG 1381
Db 571 CTGTTATTCTAGATGATTAACCTTTGTAACAAAGGCCCAATGCCCTAACCTATGACCCATATG 512
QY 1382 TAAACTACTCTCCCGCCCATACAAATCCGCCCAACCTTCTCTTACCACTCCCGTTACTTCA 1441
Db 511 TAAACTACTCTCCCGCCCATACAAATCCGCCCAACCTTCTCTTACCACTCCCGTTACTTCA 452
QY 1442 CACCCAAACCTCTTCTGACTCCACATGATTTACTTCCCAACCAATTAACAAAGGAATC 1501
Db 451 CACCCAAACCTCTTCTGACTCCACATGATTTACTTCCCAACCAATTAACAAAGGAATC 392
QY 1502 AGCTTTGATGAGGTACAAACCTCTAGAAATGTGGACCACTAGGCTCGGCATGCGT 1561
Db 391 AGCTTTGATGAGGTACAAACCTCTAGAAATGTGGACCACTAGGCTCGGCATGCGT 332
QY 1562 TCGAAAACAGTATATACGACAGGACTACAAATCCGTGTACCACTATGATGTACAAATCA 1621
Db 331 TCGAAAACAGTATATACGACAGGACTACAAATCCGTGTACCACTATGATGTACAAATCA 272
QY 1622 GAGAAATTTAATCTTAAAGACCCCCCACTTAAACCTTAAATGAATATAAATTAACCAAT 1681
Db 271 GAGAAATTTAATCTTAAAGACCCCCCACTTAAACCTTAAATGAATATAAATTAACCAAT 215
QY 1682 ACGATGTGATACAAAGAGCTCAGTAATTTATTTATATGGGAAAGGACACAGGCTG 1741
Db 214 ACGAAGTGTAT---AAAAAAGACTCAGTAATTTATTTATATGGAATTCAGGGCATGGGG 158
QY 1742 GGTCCACTGCTTCAATCGGCC 1763
Db 157 GGGAAAGGCTGACGAAGTGGCC 136

RESULT 7

ID ABX08219/c
XX ABX08219 standard; DNA; 1774 BP.
AC ABX08219;
XX
DT 20-JAN-2003 (first entry)
XX
DE PMWS-Porcine circovirus (PCV) genome.
XX
KW Porcine circovirus genome; PCV; vaccine; type I PCV strain;
KW type II PCV strain; congenital tremor; pig; whole PCV vaccine;
KW passive immunisation; ds.
XX
OS Porcine circovirus.
XX
PN WO200196377-A2.
XX
PD 20-DEC-2001.
XX
XX 15-JUN-2001; 2001WO-US019220.
XX
XX 15-JUN-2000; 2000US-0211710P.
PR (PURD) PURDUE RES FOUND.
XX
XX Mittal SK, Stevenson GW, Choi J, Kiupel M, Kanitz CL;
PI WPI; 2002-106466/14.
DR N-PSDB; ABU02907, ABU02915, ABU02920, ABU02927, ABU02936, ABU02938,
DR ABU02946, ABU02953, ABU02959, ABU02969, ABU02971.
XX
XX New porcine circovirus (PCV) nucleic acids for use as a component of
PT vaccines for treating or preventing congenital tremors in pigs.
XX
XX Example 1; Fig 1; 89pp; English.
PS
XX
XX The invention describes an isolated nucleic acid (I) from a porcine
CC circovirus (PCV) where (I) comprises a sequence coding for a circovirus
CC polypeptide. A vaccine comprising a PCV nucleic acid that encodes an

CC immunogenic polypeptide of type I or type II PCV strain and a carrier, is
CC useful for treating or preventing congenital tremors in a pig or its
CC progeny (PCV type I is composed of PK-15-PCV and CT-PCV-P7; PCV type II
CC is composed of PMWS-PCV-P1, PMWS-PCV-P2, -P3, -P4, and CT-PCV-P5, -P6).
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CC of congenital tremors in a pig which involves determining whether the pig
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CC in a biological sample from the pig, by detecting hybridisation of an
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CC by detecting the presence of PCV polypeptide in a biological sample from
CC the pig by detecting binding of an antibody that specifically binds a PCV
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CC in a biological sample of the pig. An expression vector (III) encoding a
CC PCV polypeptide is useful as a vector vaccine against congenital tremors.
CC (II) along with a suitable adjuvant is useful as a whole PCV vaccine.
CC while the antigenic PCV polypeptides are used as components of subunit
CC vaccines. Antibodies against PCV proteins are useful in passive
CC immunisation strategies. This sequence represents a porcine circovirus
CC genome
XX
SQ Sequence 1774 BP; 452 A; 364 C; 497 G; 461 T; 0 U; 0 Other;
Query Match 71.7%; Score 1270.8; DB 6; Length 1774;
Best Local Similarity 88.8%; Pred. No. 0;
Matches 1463; Conservative 0; Mismatches 157; Indels 28; Gaps 7;
QY 135 ACTGGGGCCAAAAGGAACAGTACCCCTTTAGTCTCTACAGTCAATGGATACCGTC 194
Db 1774 ACTGGGGCCAAAAGGAACAGTACCCCTTTAGTCTCTACAGTCAATGGATATCGATC 1715
QY 195 ACACAGTCTCAGTAGATCATCCCAAGGTAACAGCCATATAAATCATCCAAACCAACAC 254
Db 1714 ACACAGTCTCAGTAGATCATCCCAAGGTAACAGCCATATAAAGTCAATCAATCAACAC 1655
QY 255 TTCTTCTCCATGATATCCATCCACCACTTATTTCTACTAGGCTTCCAGTAGGTCCCT 314
Db 1654 TTCTTCAACGTGTAACCATCCACCACTTGTCTTAGGTGGTTTCCAGTATGTGTTTC 1595
QY 315 AGGCTCAGCAAAATTTACGGGCCCACTGGCTCTTCCCAACACCGGGCGGCCCATATGAC 374
Db 1594 CGGTCTGCAAAATTTAGAGGCCCATTTGCTTTTACACACCGAGTGGGCCCAATGAC 1535
QY 375 GTGTACAGCTGTCTTTCCAATCAGCTGTGATCTTCCCGCTCACTTTCAAAGTTCAGC 434
Db 1534 GTGTACATTTGCTCTTCCAATCAGCTTCTGATTTTCCCGCTCACTTTCAAAGTTCAGC 1475
QY 435 CAGCCCGGGAAAATTTCTCATAATGTTACAGGAACTGTCTCGGTACAGTACCAAGA 494
Db 1474 CAGCCCGGGAAAATTTCTGACAAACGTTACAGGGTGTGCTCTGCAACGGTCACCAAGCT 1415
QY 495 CCCGTCTCCAAAGGGTACTCACAGCAGTAGACAGGTGCGTGGCTTCCCTGGTTCCG 554
Db 1414 CCCGTCTCCAAAGGGTACTCACAGCAGTAGACAGGTGCGTGGCTTCCCTGGTTCCG 1355
QY 555 CGGAGCTCCACATCGATAAGTATGTGGCTTCTTTACTGCAAGTATCTTTATTTCTGCTG 614
Db 1354 AGGAGCTCCACATTCATTAAGTAAAGTTGCTTCTTACTGCAATATCTTTATTTCTGCTG 1295
QY 615 GTCGGTTCTTTCGTTTCTCGATGTGGCAGCGGCACCAAAATACCACTTCCCTTGT 674
Db 1294 ATCAGTTCTTTCGTTTCTCGATGTGGCAGCGGCACCAAAATACCACTTCCCTTGT 1235
QY 675 AAAAGTCTGCTTCTTAGCAAAATTCGAAACCCCTGGAGGTGAGGATTTCTACCTCTTC 734
Db 1234 GAAAGTTGCTTCTTCAAAATTTAGCGAACCCCTGGAGGTGAGGATTTCTGCTTCTCTC 1175
QY 735 CAAACCTTCTTCGCCCAACAAATATCAAAAGGGAGATTTGGAAGCTCCCGTATTTT 794
Db 1174 ATTACCTTCTTCGCCCAACAAATATCAAAAGGGAGATTTGGAAGCTCCCGTATTTT 1115
QY 795 GTTTTCTCTCTCGGAAAGGATTTAAGGGGTGAACACCCACCTCTTTATGGGGTTGCGG 854

Db 1114 CTTGCGTGTGTCGGAAGGATTATTACAGCGTGAACACCCACCTTTTATGTGTTGGG 1055
Qy 855 GCAGCTT-----TTCTGTGTGGCAATTTT---CACTGAGCTGCCAGGTGCTGC 901
Db 1054 TCCGCTTTCTTCCATCTTTGCTGGGCATGTTGCTGCTGAGGTGCTGCCAGGTGCTGC 995
Qy 902 CGCTGCCGAAGTGGCTGTAATACTACAGCAGCGCACTTCTTTCACTTTTATAGGATGA 961
Db 994 CGCTGCCGAAGTGGCTGTAATACT--TACAGCGCACTTCTTTGTTTCA-GCTATGA 938
Qy 962 CGTATCCAAGAGGCGTTTACCGCAGAAGAGACACCGCCCGCAGCCATCTTTGGCCAGA 1021
Db 937 CGTATCCAAGAGGCGTTTACCGCAGAAGAGACACCGCCCGCAGCCATCTTTGGCCAGA 878
Qy 1022 TCCTCCGCGCGCCCTGCTGCTGCTACCCCGCCACCGTACCGTTGGAGAAG--- 1077
Db 877 TCCTCCGCGCGCCCTGCTGCTGCTACCCCGCCACCGTACCGTTGGAGAAGGCC 818
Qy 1078 --AAAAATGGCATCTTCAACACCGCGCTCTCCCGCACCTTCGGATATCTGTCAAGGCTA 1135
Db 817 GAAAAATGGCATCTTCAACACCGCGCTCTCCCGCACCTTCGGATATCTGTCAAGGCTA 758
Qy 1136 CCACAGTCAGAACGCCCTCTCTGGCGGTGGACATGATGAGATTTAATATTGACACTTTG 1195
Db 757 CCACAGTCAGAACGCCCTCTCTGGCGGTGGACATGATGAGATTTAATATTGACACTTTG 698
Qy 1196 TTCCCGCGGAGGGGACCAACAAATCTCTATACCTTTGATATCTACAGATAGAA 1255
Db 697 TTCCCGCGGAGGGGACCAACAAATCTCTATACCTTTGATATCTACAGATAGAA 638
Qy 1256 AGGTTAAGGTTGAATCTGGCCCTGCTCCCGCATCACCCAGGGTGATAGGGAGTGGGCT 1315
Db 637 AGGTTAAGGTTGAATCTGGCCCTGCTCCCGCATCACCCAGGGTGATAGGGAGTGGGCT 578
Qy 1316 CCACCTGCTGTTATTCTAGATGATAACTTTGTAAACAAAGGCCACAGCCCTAACCTATGACC 1375
Db 577 CCACCTGCTGTTATTCTAGATGATAACTTTGTAAACAAAGGCCACAGCCCTAACCTATGACC 518
Qy 1376 CATATGTAACTACTCTCCCGCATCAATCCCGCACCTTCTTACCACTCCCGTT 1435
Db 517 CATATGTAACTACTCTCCCGCATCAATCCCGCACCTTCTTACCACTCCCGTT 458
Qy 1436 ACTTCACACCAACCTGTTCTTCACTCCACATTTGATTCTTCAACCAATAACAAAA 1495
Db 457 ACTTCACACCAACCTGTTCTTCACTCCACATTTGATTCTTCAACCAATAACAAAA 398
Qy 1496 GGAATCAGCTTTGATGAGGTACAAAACCTCTAGAAATGTGGACCAAGTGGCTCGGCA 1555
Db 397 GGAATCAGCTTTGATGAGGTACAAAACCTCTAGAAATGTGGACCAAGTGGCTCGGCA 338
Qy 1556 CTGGCTTCGAAAACAGTATATACACAGGACTACAAATCCCGTGAACCATGTATGTAC 1615
Db 337 CTGGCTTCGAAAACAGTATATACACAGGACTACAAATCCCGTGAACCATGTATGTAC 278
Qy 1616 AATTTCAGAGATTTAATCTTAAAGACCCCGCACCTTAAACCCCTTAATGAATAAATAAAA 1675
Db 277 AATTTCAGAGATTTAATCTTAAAGACCCCGCACCTTAAACCCCTTAATGAATAAATAAAA 221
Qy 1676 ACCATTACGATGTGATTAACAAAAAGACTCAGTAAATTTATTTATTTATGGAAAAAGGCA 1735
Db 220 ACCATTACGAGTGTAT--AAAAAGACTCAGTAAATTTATTTATTTATTTATGGAAAAAGGCA 164
Qy 1736 AGGTGGGTCCAGCTCTTCAATCGGC 1763
Db 163 ATGGGGGGGAAGGGTGACGAACCTGGGC 136

RESULT 8
ABX08202/c
ID ABX08202 standard; DNA; 1762 BP.
XX
AC ABX08202;

XX 20-JAN-2003 (first entry)
DT
XX PWMS-Porcine circovirus (PCV) P1 genome.
DE
XX Porcine circovirus genome; PCV; vaccine; type I PCV strain;
KW type II PCV strain; congenital tremor; pig; whole PCV vaccine;
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XX Porcine circovirus.
OS
XX WO200196377-A2.
PN
XX 20-DEC-2001.
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XX 15-JUN-2000; 2000US-0211710P.
PR
XX (PURD) PURDUE RES FOUND.
PA
XX Mittal SK, Stevenson GW, Choi J, Kiupel M, Kanitz CL;
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XX WPI; 2002-106466/14.
DR N-PSDB; ABU02908, ABU02913, ABU02917, ABU02924, ABU02931, ABU02941,
DR ABU02943, ABU02950, ABU02957, ABU02965.
XX
XX New porcine circovirus (PCV) nucleic acids for use as a component of
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XX Claim 1; Page 82; 88pp; English.
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XX The invention describes an isolated nucleic acid (I) from a porcine
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CC polypeptide. A vaccine comprising a PCV nucleic acid that encodes an
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CC useful for treating or preventing congenital tremors in a pig or its
CC progeny [PCV type I is composed of PK-15-PCV and CT-PCV-P7; PCV type II
CC is composed of PWMS-PCV-P1, PWMS-PCV-P2, -P3, -P4, and CT-PCV-P5, -P6].
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CC the infection is effected by detecting the presence of a PCV nucleic acid
CC in a biological sample from the pig, by detecting hybridisation of an
CC oligonucleotide. Optionally, the determination of infection is effected
CC by detecting the presence of PCV polypeptide in a biological sample from
CC the pig by detecting binding of an antibody that specifically binds a PCV
CC polypeptide. Optionally, the determination of infection is effected by
CC detecting the presence of antibodies directed against a PCV polypeptide
CC in a biological sample of the pig. An expression vector (III) encoding a
CC PCV polypeptide is useful as a vector vaccine against congenital tremors.
CC (II) along with a suitable adjuvant is useful as a whole PCV vaccine,
CC while the antigenic PCV polypeptides are used as components of subunit
CC vaccines. Antibodies against PCV proteins are useful in passive
CC immunisation strategies. This sequence represents a porcine circovirus
CC genome
XX
SQ Sequence 1762 BP; 450 A; 359 C; 492 G; 461 T; 0 U; 0 Other;

Query Match 70.6%; Score 1252; DB 6; Length 1762;
Best Local Similarity 88.2%; Pred. No. 0;
Matches 1449; Conservative 0; Mismatches 165; Indels 28; Gaps 7;
Qy 135 ACTCGGGGCCAAAAAGAACAGTACCCTTTAGTCTCTACAGTCAATGATACCGGTC 194
Db 1762 ACTCGGGGCCAAAAAGAACAGTACCCTTTAGTCTCTACAGTCAATGATACGATC 1703
Qy 195 ACACAGTCTCAGTAGATCATCCCAAGGTAAACCGCCATAAAAAATCATCCAAAAACAAC 254
Db 1702 ACACAGTCTCAGTAGATCATCCCAAGGTAAACCGCCATAAAAAATCATCAATAACAC 1643
Qy 255 TTCTTCTCCATGATATCCATCCCAAGGTAAATTTTCTTACTAGGCTTCCAGTAGGTGTCCT 314

Db 1642 TTCTTCCATGTTAAACCATCCACCACTTGTCTTAGGTGTTTCCAGTATGTGGTTTC 1583
 Qy 315 AGGCTCAGCAAAATTAACGGGCCACTGGCTCTTCCACAACGGGGCGGCCCACTATGAC 374
 Db 1582 CGGGTCTGCAAAATTTAGCAGCCCAATTTGCTTTTACCAACACCGAGTGGCCCAATGAC 1523
 Qy 375 GTGTACAGCTGTCTTCCATCAGCTGTGCTGATCTTCCGGCTCACTTTCAAAAGTTGACG 434
 Db 1522 GTGTACATGTGTTCTTCCCAATCAGCTGTGCTGATCTTCCGGCTCACTTTCAAAAGTTGACG 1463
 Qy 435 CAGCCCGGGGAAATTTCTCACATACGTTTACAGGAACTGTCTGGCTCAGTCCACCAAGA 494
 Db 1462 CAGCCCGGGGAAATTTCTGCAAAAGTTTACAGGGTGTCTCTGCAACGGTCAACGACT 1403
 Qy 495 CCGCGTCTCCAAAGGGTACTCACAGCAGTAGACAGGTGCTGCGCTTCCCGCTGGTTCCG 554
 Db 1402 CCGCGTCTCCAAAGGGTACTCACAGCAGTAGACAGGTGCTGCGCTTCCCGCTGGATCG 1343
 Qy 555 CGGAGCTCCACACTCGATAAGTATGTGGCTTCTTACTGCAAGTATCTTTATTTCTGCTG 614
 Db 1342 AGGAGCTCCACATTCATTAAGTAAGTTGCTTCTTACTGCAATATCTTTATTTCTGCTG 1283
 Qy 615 GTGCTTCTCTTCTGCTTCTGATGTGGCAGCGGSCACCAAAATACCACTTTCACCTGTT 674
 Db 1282 ATCAGTTCCTTGGCTTCTGATGTGGCAGCGGSCACCAAAATACCACTTTCACCTTAT 1223
 Qy 675 AAAAGTCTGCTTCTTAGCAAAATTCGCAAAACCCCTGGAGGTGAGGAGTTCTACCTCTTC 734
 Db 1222 AAAAGTTCCTTCTTACAAAATTAGCGAAACCCCTGGAGGTGAGGTGCTGCTCTCTC 1163
 Qy 735 CAAACCTTCTCGGCCAACAACAAATATCAAAAGGGAGATTGGAAGCTCCCGTATTTT 794
 Db 1162 ATTACCTCTCTCGCCAAACAATAAATAATCAATAGGGAGATTGGGAGCTCCCGTATTT 1103
 Qy 795 GTTTTCTCTCTCTCGGAGGATTAATTAAGGTGGAACACCCACCTCTTATGGGTGCGG 854
 Db 1102 ATTGGCTGCTTCTGGAGGATTAATCAGCGTGAACACCCACCTTTTATGGGTGGG 1043
 Qy 855 GCCGCTT-----TTCTTGTCTGGCAATTT-----CACTGACGCTGCCGAGTGTGTC 901
 Db 1042 TCCGCTTCTTCCATTTCTTGTCTGGGCATGTGTCTGTGAGGTGCTGCGAGGTGCTGC 983
 Qy 902 CGTGTCCGAAGTGGCTGTTAATTAATAACAGAGCGCACTTCTTCACTTTTATAGTAGA 961
 Db 982 CGTGTCCGAAGTGGCTGTTAATACT--TACAGGCACTTCTTTC-GTTTTCAGTATGA 926
 Qy 962 CGTATCCAAGAGAGGCTTACCGCAGAGAAGACACCGCCCGCAGCCATCTTGGCCAGA 1021
 Db 925 CGTATCCAAGAGAGGCTTACCGCAGAGAAGACACCGCCCGCAGCCATCTTGGCCAGA 866
 Qy 1022 TCCTCCGCGCGCCCTGCTGCTCCACCCCGCCACCGCTACCGTTGGAGAGAGGAAA 1081
 Db 865 TCCTCCGCGCGCCCTGCTGCTCCACCCCGCC-----ACGTTGGAGAGGAAA 812
 Qy 1082 ATGGGATCTTCAACACCGGCTCTCCCGCACTTCCGATATCTGTCAAGGCTACCAAG 1141
 Db 811 ATGGCATCTTCAACACCGGCTCTCCCGCACTTCCGATATCTGTCAAGGCTACCAAG 752
 Qy 1142 TCAGAACGCTCTCTGGCGGTGACATGATGAGATTTAATTTGACGACTTTGTTCCCC 1201
 Db 751 TCAGAACGCTCTCTGGCGGTGACATGATGAGATTTAAGCTTTGACGACTTTGTTCCCC 692
 Qy 1202 CGGAGGGGGGACCAACAAAATCTCTATACCTTTTGAATACTACAGATAAGAAAGTTA 1261
 Db 691 CGGAGGGGGGACCAACAAAATCTCTATACCTTTTGAATACTACAGATAAGAAAGTTA 632
 Qy 1262 AGGTTGAATTTCTGGCTGCTCCCGCATCAACCGAGGTGATAGGGAGTGGCTTCCACTG 1321
 Db 631 AGGTTGAATTTCTGGCTGCTCCCGCATCAACCGAGGTGATAGGGAGTGGCTTCCACTG 572
 Qy 1322 CTGTTATCTAGATGATACTTTGTAACAAAGGCCACAGCCCTAACCTATGACCCATATG 1381
 Db 571 CTGTTATCTAGATGATACTTTGTAACAAAGGCCAAATGCCCTAACTATGACCCATATG 512

Qy 1382 TAAACTACTCTCCCGCCATACAATCCCCCAACCCCTTCTCTACACTCCCGTTACTTCA 1441
 Db 511 TAAACTACTCTCCCGCCATACAATCCCCCAACCCCTTCTCTACACTCCCGTTACTTCA 452
 Qy 1442 CACCCAACTGTTCTTGGACTCCACCATTGATTTACTTCCCAACCAATACCAAGGAATC 1501
 Db 451 CACCCAACTGTTCTTGGACTCCACCATTGATTTACTTCCCAACCAATACCAAGGAATC 392
 Qy 1502 AGCTTTGGATGAGGCTACAAACCTCTAGAAAATGGGACACGCTAGGCTTCGGCTGCGT 1561
 Db 391 AGCTTTGGCTGAGGCTACAAACCTCTAGAAAATGGGACACGCTAGGCTTCGGCTGCGT 332
 Qy 1562 TCGAAAACAGTATATACGACGAGACTACAATATCCGTTAAACCATGTATGTACAATTCA 1621
 Db 331 TCGAAAACAGTATATACGACGAGACTACAATATCCGTTAAACCATGTATGTACAATTCA 272
 Qy 1622 GAGATTTAATCTTAAAGACCCCCCACTTAAACCTTAATGAATATAAATAAARACCAATT 1681
 Db 271 GAGATTTAATCTTAAAGACCCCCCACTTAAACCTTAATGAATATAAATAAARACCAATT 215
 Qy 1682 ACGATGTATAACAAAAAGACTCAGTAATTTATTTATATGGGAAAAGGCGACAGGCTG 1741
 Db 214 ACGAAGTAT---AAAAAGACTCAGTAATTTATTTATATGGGAAAAGGCGACAGGCTG 158
 Qy 1742 GGTCCACTGCTTCAAAATCGGCC 1763
 Db 157 GGGAAAGGGTGACGAACTGGCC 136

RESULT 9

ABX08208/c

ID ABX08208 standard; DNA; 1759 BP.

XX AC ABX08208;

XX XX 20-JAN-2003 (first entry)

XX DE CT-Porcine circovirus (PCV) P7 genome.

XX KW Porcine circovirus genome; PCV; vaccine; type I PCV strain;

XX KW type II PCV strain; congenital tremor; pig; whole PCV vaccine;

XX KW passive immunisation; ds.

XX OS Porcine circovirus.

XX PN WO200196377-A2.

XX PD 20-DEC-2001.

XX PF 15-JUN-2001; 2001WO-US019220.

XX PR 15-JUN-2000; 2000US-0211710P.

XX PA (PURD) PURDUE RES FOUND.

XX PI Mittal SK, Stevenson GW, Choi J, Kiupel M, Kanitz CL;

XX XX WPI; 2002-106466/14.

XX DR New porcine circovirus (PCV) nucleic acids for use as a component of

XX PT vaccines for treating or preventing congenital tremors in pigs.

XX PS Claim 1; Page 86; 88pp; English.

The invention describes an isolated nucleic acid (I) from a porcine
 circovirus (PCV) where (I) comprises a sequence coding for a circovirus
 polypeptide. A vaccine comprising a PCV nucleic acid that encodes an
 immunogenic polypeptide of type I or type II PCV strain and a carrier, is
 useful for treating or preventing congenital tremors in a pig or its
 progeny (PCV type I is composed of PK-15-PCV and CT-PCV-P7; PCV type II
 is composed of PMWS-PCV-P1, PMWS-PCV-P2, -P3, -P4, and CT-PCV-P5, -P6).
 An isolated PCV strain (II) is useful for diagnosing a pathological cause

CC of congenital tremors in a pig which involves determining whether the pig
CC has been infected by PCV strain type I or type II. The determination of
CC the infection is effected by detecting the presence of a PCV nucleic acid
CC in a biological sample from the pig, by detecting hybridisation of an
CC oligonucleotide. Optionally, the determination of infection is effected
CC by detecting the presence of PCV polypeptide in a biological sample from
CC the pig by detecting binding of an antibody that specifically binds a PCV
CC polypeptide. Optionally, the determination of infection is effected by
CC detecting the presence of antibodies directed against a PCV polypeptide
CC in a biological sample of the pig. An expression vector (III) encoding a
CC PCV polypeptide is useful as a vector vaccine against congenital tremors.
CC (ii) along with a suitable adjuvant is useful as a whole PCV vaccine,
CC while the antigenic PCV polypeptides are used as components of subunit
CC vaccines. Antibodies against PCV proteins are useful in passive
CC immunisation strategies. This sequence represents a porcine circovirus
CC genome
XX

SQ Sequence 1759 BP; 430 A; 347 C; 508 G; 474 T; 0 U; 0 Other;

Query Match 68.7%; Score 1218.2; DB 6; Length 1759;
Best Local Similarity 85.2%; Pred. No. 0;
Matches 1402; Conservative 0; Mismatches 223; Indels 20; Gaps 3;

Qy 135 ACTGCGGCGCAAAAGGAACAGTACCCCTTTAGTCTCTACAGTCAATGGATACCGGTC 194
Db 1759 ACTGCGGCGCAAAAGGAACAGTACCCCTTTAGTCTCTACAGTCAATGGATACCGGTC 1700
Qy 195 ACACAGTCTCAGTAGATCATCCCAAGGTAAACGCCATATAAATCATCCAAACAAAC 254
Db 1699 ACACAGTCTCAGTAGATCATCCCAAGGTAAACGCCATATAAATCATCCAAACAAAC 1640
Qy 255 TTCTTCTCCATGATATCCATCCACCACTTATTTCTACTAGGCTTCCAGTAGGTCCCT 314
Db 1639 TTCTTCTCCATGATATCCATCCACCACTTATTTCTACTAGGCTTCCAGTAGGTCCCT 1580
Qy 315 AGGCTCAGCAAAATTAACGGGCCCACTGGCTCTTCCCAACACCGGGCGGCCCATATGAC 374
Db 1579 AGGCTCAGCAAAATTAACGGGCCCACTGGCTCTTCCCAACACCGGGCGGCCCATATGAC 1520
Qy 375 GTGTACAGTGTCTTCAATCAGCTGCTGCACTCTCCCGTCACTTTTCAAAAGTTGACG 434
Db 1519 GTGTACAGTGTCTTCAATCAGCTGCTGCACTCTCCCGTCACTTTTCAAAAGTTGACG 1460
Qy 435 CAGCCCGCGGAATTTCTCATACAGTTTACAGGAACCTGCTCGGCTACAGTCAACCAAGA 494
Db 1459 CAGCCCGCGGAATTTCTCATACAGTTTACAGGAACCTGCTCGGCTACAGTCAACCAAGA 1400
Qy 495 CCGCGTCTCCAAAGGGTACTCACAGCAGTAGACAGTCTGCTGCGCTTCCCTGGTTCCG 554
Db 1399 CCGCGTCTCCAAAGGGTACTCACAGCAGTAGACAGTCTGCTGCGCTTCCCTGGTTCCG 1340
Qy 555 CGGAGCTCCACATCGATAGTATGGCGCTTCTTTACTGAGTATCTTTATCTGCTG 614
Db 1339 CGGAGCTCCACATCGATAGTATGGCGCTTCTTTACTGAGTATCTTTATCTGCTG 1280
Qy 615 GTGCGTTCTTTTGGCTTCTCGATGTGCGCGGGCACAAATPACCACTTTTCACTTTGT 674
Db 1279 GTGCGTTCTTTTGGCTTCTCGATGTGCGCGGGCACAAATPACCACTTTTCACTTTGT 1220
Qy 675 AAAAGTCTGCTCTTAGCAAAATTCGAAACCCCTGGAGGTGAGGAGTTCTTACCTCTTC 734
Db 1219 AAAAGTCTGCTCTTAGCAAAATTCGAAACCCCTGGAGGTGAGGAGTTCTTACCTCTTC 1160
Qy 735 CAAACCTCTCGGCACAAACAAATTAATCAAAAGGGAGATTGGAAAGCTCCCGTATTTT 794
Db 1159 CAAACCTCTCTCCACAAACAAATTAATCAAAAGGGAGATTGGAAAGCTCCCGTATTTT 1100
Qy 795 GTTTTCTCTCTCGGAAGGATTTAAGGGTCAACACCCACCTCTTTATGGGGTTCGG 854
Db 1099 GTTTTCTCTCTCGGAAGGATTTAAGGGTCAACACCCACCTCTTTATGGGGTTCGG 1040
Qy 855 GCCGCTTTCTGCTTGGCAATTTTCACTGACGCTGCCGAGGTGTGCGCTGCCGAAGTG 914

Db 1039 GCCTCTTTCTGCTGGCATTTTCACTGACGCTGCCGAGGTGCTGCCGTGCCGAAGTG 980
Qy 915 CGCTGGTAATACCTACAGCAGCGCACTTCTTTCACTTTTATAGATGACGTATCAAGGAG 974
Db 979 CGCTGGTAATACCTACAGCAGCGCACTTCTTTCACTTTTATAGATGACGTGGCAAGGAG 920
Qy 975 GCCTTACCGCAGGAAGAAGACACCGCCCGCCAGCCATCTTTGGCCAGATCTCCGCCCGCG 1034
Db 919 GCCTTACCGCAGGAAGAAGGACCGCCCGCCAGCCATCTTTGGAAACATCTCCCGGAGAAG 860
Qy 1035 CCCCTGGCTCGTCCACCC-----CGCCACCGCTACCGTTGGAGAGGAAAGAAATGCGAT 1088
Db 859 ACCATATTTGGTACACCCCGCTTTCAGAAACCGTTACAGATGGCGCCGAAAGAGGTAT 800
Qy 1089 CTTCAACACCGCGCTCTCCCGACCTTCGGATATATCTGTCAGAGCTACCAAGCTCAGATCAGAAC 1148
Db 799 CTTCAATTTCCCGCTTTCTTAGAGAAATTTGTAATCTACCATATAAG---GAGGACACTCGCA 743
Qy 1149 GCCTCTCTGGCGGTGGACATGATGATTAATATTGACGACTTTTGTTCCTCCCGGGAGG 1208
Db 742 GCCATCTTGGAAATGTTAACCACTCAGATTCAACATCGGCCAGTTCTCTCCCGCTCGG 683
Qy 1209 GGGGACCAACAAATCTCTATACCTTTGAAATCTACAGAAATAGAAAGGTAAAGTTGA 1268
Db 682 CGGCACCAACCCCGCTACCCCTACCTTTTCCAATATACCGTATTAGAAAGGCTAAATATGA 623
Qy 1269 ATTCTGGCCCTGCTCCCGCATCCAGGGGTAGAGGGAGTGGGCTCCACTGCTGTTAT 1328
Db 622 ATTTTACCCAGAGAGACCCCATCACCCTTAATCAAGAGGTGTAGGTTCCACTGTTGTTAT 563
Qy 1329 TCTAGATGATAACTTTGTAAACAAAGGCCACAGCGCTTAACCTATGACCCATATGTAAACTA 1388
Db 562 CTTGGATGCCAACTTTGTAAACCCCTCCACCAACCTGGCTATGACCCCTATATACTA 503
Qy 1389 CTCTCCCGCCTACCAATATCCCAACCCCTTCTCTACCTCCGCTTCTTCTACACCCAA 1448
Db 502 CTCTCCCGCCTACCAATATAGGCAACCCCTTTACCTACCTCCAGGTACTTCAACCCCAA 443
Qy 1449 ACCTGTTCTTGTACTCCACCAATGATTTCTTCCAAACCAATAACAAAGGAATCAGCTTTG 1508
Db 442 ACCTGAGCTGGACCAACAAATTTGATTTGGTTCCAGCCAAATAATAAAGAAACCAAGCTGTG 383
Qy 1509 GATGAGGCTACAAACCTCTAGAAATTTGGACACCTAGGCTCGGCACTCGGTTTCAAAAA 1568
Db 382 GCTCCATTTAAATACCCACCAATATGTCGAGCACAGGCTCGGCTTTGCGCTCCAAA 323
Qy 1569 CAGTATATACGACGAGGACTACAAATATCCGTTGTAACCATGTATGTACAAATTCAGAGATT 1628
Db 322 TGCAGACACAGCCCAAAATTTATGTGGTAAGGCTGACTATTTATGTACAAATTCAGAGATT 263
Qy 1629 TAATCTTAAAGACCCCGCACTTAAACCCCTAAATGAATAAATAAATAAATAAATACGATGT 1688
Db 262 TATCTGAAAGACCC-----CTCTAAATGAATAAATAAATAAATAAATACGATGT 214
Qy 1689 GATAACAAAAAGACTCAGTAATTTTATTTTATATGGGAAAGGGCACAGGGTGGGTCCAC 1748
Db 213 GATAACAAAAAGACTCAGTAATTTTATTTTATATGGGAAAGGGCACAGGGTGGGTCCAC 154
Qy 1749 TGCTTCAATCGCGCTTCGGGTACC 1773
Db 153 TGCTTCAATCGCGCTTCGGGTACC 129

RESULT 10
ABX08220/c
ID ABX08220 standard; DNA; 1759 BP.
XX AC ABX08220;
XX AC AC
XX AC AC
DT 20-JAN-2003 (first entry)
XX DE PK-15-Porcine circovirus (PK-15-PCV) genome.
XX

Porcine circovirus genome; PCV; vaccine; type I PCV strain;
type II PCV strain; congenital tremor; pig; whole PCV vaccine;
passive immunisation; db.

Porcine circovirus.

W0200196377-A2.

20-DEC-2001.

15-JUN-2001; 2001WO-US019220.

15-JUN-2000; 2000US-0211710P.

(PURDUE RES FOUND.

Mittal SK, Stevenson GW, Choi J, Kiupel M, Kanitz CL;

WPI; 2002-106466/14.

N-FSDB; AB02909, AB02916, AB02923, AB02930, AB02949, AB02956.

New porcine circovirus (PCV) nucleic acids for use as a component of
vaccines for treating or preventing congenital tremors in pigs.

Example 1; Fig 1; 89pp; English.

The invention describes an isolated nucleic acid (I) from a porcine
circovirus (PCV) where (I) comprises a sequence coding for a circovirus
polypeptide. A vaccine comprising a PCV nucleic acid that encodes an
immunogenic polypeptide of type I or type II PCV strain and a carrier, is
useful for treating or preventing congenital tremors in a pig or its
progeny (PCV type I is composed of PK-15-PCV and CT-PCV-P7; PCV type II
is composed of PMS-PCV-P1, PMS-PCV-P2, -P3, -P4, and CT-PCV-P5, -P6).
An isolated PCV strain (II) is useful for diagnosing a pathological cause
of congenital tremors in a pig which involves determining whether the pig
has been infected by PCV strain type I or type II. The determination of
the infection is effected by detecting the presence of a PCV nucleic acid
in a biological sample from the pig, by detecting hybridisation of an
oligonucleotide. Optionally, the determination of infection is effected
by detecting the presence of PCV polypeptide in a biological sample from
the pig by detecting binding of an antibody that specifically binds a PCV
polypeptide. Optionally, the determination of infection is effected by
detecting the presence of antibodies directed against a PCV polypeptide
in a biological sample of the pig. An expression vector (III) encoding a
PCV polypeptide is useful as a vector vaccine against congenital tremors.
(II) along with a suitable adjuvant is useful as a whole PCV vaccine,
while the antigenic PCV polypeptides are used as components of subunit
vaccines. Antibodies against PCV proteins are useful in passive
immunisation strategies. This sequence represents a porcine circovirus
genome

Sequence 1759 BP; 432 A; 342 C; 510 G; 475 T; 0 U; 0 Other;

Query Match 68.3%; Score 1210.2; DB 6; Length 1759;
Best Local Similarity 84.9%; Pred. No. 0;
Matches 1397; Conservative 0; Mismatches 228; Indels 20; Gaps 3;

135 ACTGGGCGCCAAAAGGAAAGGACAGTACCCCTTTAGTCTCTCAGTCAATGATACCGGTC 194
1759 ACTGGGCGCCAAAAGGAAAGGAAAGGACAGTACCCCTTTAGTCTCTCAGTCAATGATACCGGTC 1700
195 ACACAGTCTCAGTAGATCATCCCAAGGTAACAGCCATATAAATAATCATCCAAAACAAC 254
1699 ACACAGTCTCAGTAGATCATCCCAAGGTAACAGCCATATAAATAATCATCCAAAACAAC 1640
255 TTCTTCTCCATGATATCCATCCACCACTTATTTCTACTAGGCTTCCAGTAGGTGTCCT 314
1639 TTCTTCTCCATGATATCCATCCACCACTTATTTCTACTAGGCTTCCAGTAGGTGTCCT 1580
315 AGGCTCAGCAAAATTTACGGGGCCCACTGGCTCTTCCCAACCGGGGGCCCACTATGAC 374
1579 AGGCTCAGCAAAATTTACGGGGCCCACTGGCTCTTCCCAACCGGGGGCCCACTATGAC 1520

Qy 375 GTGTACAGCTGTCTTCCATCAGCTGTGTGATCTTCCCGCTCATTTCACAAAGTTTCAGC 434
Db 1519 GTGTACAGCTGTCTTCCATCAGCTGTGTGATCTTCCCGCTCATTTCACAAAGTTTCAGC 1460
Qy 435 CAGCCGCGGAAATTTCTCACAATAGCTTTACAGGAACTGTCTCGCTCAGTCACCAAGA 494
Db 1459 CAGCCGCGGAAATTTCTCACAATAGCTTTACAGGAACTGTCTCGCTCAGTCACCAAGA 1400
Qy 495 CCCCCTTCCAAAAGGTAATTCACAGCAGTAGACAGGTCTGTGCGCTTCCCTGGTTCCG 554
Db 1399 CCCCCTTCCAAAAGGTAATTCACAGCAGTAGACAGGTCTGTGCGCTTCCCTGGTTCCG 1340
Qy 555 CGGAGCTCCACATCGATAGTATGTGGCTTCTTACTGCAATATCTTATTTCTGCTG 614
Db 1339 CGGAGCTCCACATCGATAGTATGTGGCTTCTTACTGCAATATCTTATTTCTGCTG 1280
Qy 615 GTCCGTTCTCTTTCGCTTCTCGATGTGGCAGCGGCACAAAATACCACTTCCACCTGTT 674
Db 1279 GTCCGTTCTCTTTCGCTTCTCGATGTGGCAGCGGCACAAAATACCACTTCCACCTGTT 1220
Qy 675 AAAAGTCTGCTTCTTAGCAAAATTCGAAACCCCTGGAGGTGAGAGTTCTACCCCTCTC 734
Db 1219 AAAAGTCTGCTTCTTAGCAAAATTCGAAACCCCTGGAGGTGAGAGTTCTACCCCTCTC 1160
Qy 735 CAAACCTTCTCTCGCACAACAATAATCAAAAGGAGATTTGGAAGCTCCCGTATTTT 794
Db 1159 CAAACCTTCTCTCGCACAACAATAATCAAAAGGAGATTTGGAAGCTCCCGTATTTT 1100
Qy 795 GTTTTCTCTCTCTCGGAGGATTAATTAAGGTGAAACACCCACCTCTTATGGGTTGCGG 854
Db 1099 GTTTTCTCTCTCTCGGAGGATTAATTAAGGTGAAACACCCACCTCTTATGGGTTGCGG 1040
Qy 855 GCCGCTTCTTGTCTGGCAATTTTCACTGACGCTGCCGAGGTGCTGCGCTGCCGAAGTG 914
Db 1039 GCCGCTTCTTGTCTGGCAATTTTCACTGACGCTGCCGAGGTGCTGCGCTGCCGAAGTG 980
Qy 915 CGCTGGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 974
Db 979 CGCTGGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 920
Qy 975 CGCTTACCGGAGAGAGACACCGCCCGCAGGCATCTTGGCCAGATCTCCGCGCGCG 1034
Db 919 CGCTTACCGGAGAGAGAGACCGCCCGCAGGCATCTTGGCCAGATCTCCGCGCGCG 860
Qy 1035 CCCCCTGCTCGTCCACCC-----CCGCCACCGCTACCGTTGGAGAGGAAATTTGGCAT 1088
Db 859 ACCATATTTGGCACACCGCTTTCAGAAACCGTTACAGATGGCGCCGAAAGACGGGTAT 800
Qy 1089 CTTCAACACCGCGCTCTCCCGCACCTTCGGATATATCTGTCAAGGCTACCACAGTCAGAAC 1148
Db 799 CTTCAATTTCCGCGCTTCTTACAGAAATTTGTACTCACCATAAAG---GAGGATACTCGCA 743
Qy 1149 GCCCTCTGGGCGGTGGACATGATGAGATTTAATTAATTAATTAATTAATTAATTAATTAAT 1208
Db 742 GCCATTTGGAAATTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 683
Qy 1209 GGGGACCAACAAATCTTATACCTTTTGAATTAATTAATTAATTAATTAATTAATTAATTAAT 1268
Db 682 CGGCACCAACCCCTACCTTCCCTTCCATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 623
Qy 1269 ATTCTGGCGCTCTCCCGCATACCCAGGGGTAGTAGGGAGTGGGCTCCACTGCTGTTAT 1328
Db 622 ATTTTACCCAGAGACCCCATCACCTCTAATCAAGAGGTGTTGGGCTCCACTGTTGTTAT 563
Qy 1329 TCTAGATGATTAATTTCTAAAGGCGCACAGCCCTAACCTATGACCCCATATGAACTA 1388
Db 562 CTTGGATGCCAATTTTGTAAACCCCTCCACCACTTGGCTTATGACCCCTATATTAATTAATTAAT 503
Qy 1389 CTCCTCCCGGCATCAATATCCCAACCTTCTCTACACCTTCCCGTTACTTTCACACCCAA 1448
Db 502 CTCCTCCCGGCATCAATATGAGGAGCCCTTTACCTCACTCCAGGTACTTCAACCCCAA 443
Qy 1449 ACCTGTTCTTGACTCCACCATTTGATTAATTTCCCAACCAAAATAAAGGAATACGCTTTG 1508

Qy 301 CAGTAGGTGTCCTAGGCTCAGCAAAATTAAGGCGCCACTGGCTCTTCCACCAACCGGC 360
 Db 1265 CAGTAGGTGTCCTAGGCTCAGCAAAATTAAGGCGCCACTGGCTCTTCCACCAACCGGC 1206
 Qy 361 GGGCCCACTATGAGCTGTACAGCTGTCTTCAATCAGCTGTCTGCAATCTTCCGCTCACT 420
 Db 1205 GGGCCCACTATGAGCTGTACAGCTGTCTTCAATCAGCTGTCTGCAATCTTCCGCTCACT 1146
 Qy 421 TTCAAAAGTTAGCAGCCCGCGGAAATTTCTCAGATACGTTACAGAAACTGCTCGCT 480
 Db 1145 TTCAAAAGTTAGCAGCCCGCGGAAATTTCTCAGATACGTTACAGAAACTGCTCGCT 1086
 Qy 481 ACAGTACCAAGAACCCCGTCTCCAAAGGCTACTCAGCAGTAGACAGTGTCTGCGC 540
 Db 1085 ACAGTACCAAGAACCCCGTCTCCAAAGGCTACTCAGCAGTAGACAGTGTCTGCGC 1026
 Qy 541 TTCCCTCGGTTCCGCGAGCTCCACACTCGATAGTAGTGCGCTCTTTTA-----CTG 594
 Db 1025 TTCCCTCGGTTCCGCGAGCTCCACACTCGATAGTAGTGCGCTCTTTTACTGCGCTG 966
 Qy 595 CAGTATTTCTTATCTGCTGGTTCGGTTCCTTTCGCTTCTCGATGCGAGCGGACCA 654
 Db 965 CAGTATTTCTTATCTGCTGGTTCGGTTCCTTTCGCTTCTCGATGCGAGCGGACCA 906
 Qy 655 AAATACCACCTTCACTTGTAAAGTCTGCTTCTTAGCAAAATTCGCAAAACCCCTGGAG 714
 Db 905 AAATACCACCTTCACTTGTAAAGTCTGCTTCTTAGCAAAATTCGCAAAACCCCTGGAG 846
 Qy 715 TGAGGAGTTTACCTCTTCCAAACCTTCTCGCCCAAAACAAATTAATCAAAAGGAG 774
 Db 845 TGAGGAGTTTACCTCTTCCAAACCTTCTCGCCCAAAACAAATTAATCAAAAGGAG 786
 Qy 775 ATTGGAAGCTCCGATTTTGTCTTCTCTCTCGGAAGATTAATTAAGGTGAACACC 834
 Db 785 ATTGGAAGCTCCGATTTTGTCTTCTCTCTCGGAAGATTAATTAAGGTGAACACC 726
 Qy 835 CACCTCTTATGGGTTGCGGCGCTTCTTCTGCTGGCATTTTCACTGACGCTGCGCGAG 894
 Db 725 CACCTCTTATGGGTTGCGGCGCTTCTTCTGCTGGCATTTTCACTGACGCTGCGCGAG 666
 Qy 895 GTGTCGCGTCCGAAAGTGGTGTAACTACACAGCGCACTTCTTTCACTTTAT 954
 Db 665 GTGTCGCGTCCGAAAGTGGTGTAACTACACAGCGCACTTCTTTCACTTTAT 606
 Qy 955 AGGATGAGTATCAAGAGGCGTTACGCGAGAGAGACACCGCCCGCGAGCCATCTT 1014
 Db 605 AGGATGAGTATCAAGAGGCGTTACGCGAGAGAGAGACCGCCCGCGAGCCATCTT 546
 Qy 1015 GGCCAGATCTCCGCGCGCGCTGCTGCTGCCACCC-----CCGCCACCGCTACCGT 1068
 Db 545 GGAAACATCTCCGCAAGACCATATTTGGCACACCCCGCTTCAGAAACCGTTACAGA 486
 Qy 1069 TGGAGAGGAAATAGGATCTTCAACACCGCTCTCCCGACCTTCGGATATCTGTC 1128
 Db 485 TGGCGCGAAAGACGGGTATCTTCAATTTGCGCTCTTATAGAGATTTGTACTCAC---C 429
 Qy 1129 AAGCTACCAAGTACAGACGCTCTGCGGCTGTCATGATGAGATTTAATTGAC 1188
 Db 428 ATAGAAGAGGACACTCGAGCCATCTTGGAAATGTTAAACAGCTCAGATTCACATCGGC 369
 Qy 1189 GACTTTGTCCTCCCGGAGGGGACCAACAAATCTCTATACCTTTTGAATACACAGA 1248
 Db 368 CAGTTCTCTCCCTCAGGCGGACCAACCCCTACCTTCCATCTACCTACCGT 309
 Qy 1249 ATAGAAGGTTAAGTTGAATTCGCGCTGCTCCCGCATCACCGGTTGATAGGGA 1308
 Db 308 ATAGAAGGTTAATATGAATTTTACCCAGAGACCCCATCTCTTAATCAAGAGGT 249
 Qy 1309 GTGGGCTCCACTGCTGTTATCTAGATGATTAATTTGTAACAAAGGCCACAGCCCTAAC 1368
 Db 248 GTGGGCTCCACTGCTGTTATCTTGATGCCAACTTTGTAACCCCTCACCACCTTGCC 189

Qy 1369 TATGACCCATATGTAATTAATCTCTCCCGCCATCAATAATCCCAAGCCCTTCTCTACAC 1428
 Db 188 TATGACCCCTATATTAATTAATCTCTCCCGCCATCAATAAGGCGCCCTTTACTCTACAC 129
 Qy 1429 TCCGTTTACTTACACCCAAACCTTCTTGACTCCACCAATTTGATTACTTTCGAACCAAT 1488
 Db 128 TCCAGGTACTTCAACCCCAACCTGAGCTGGACCAACCAATTTGATTGGTTCCAGCCAAAT 69
 Qy 1489 AACAAAGGAATCAGCTTTGGATGAGGCTACAAACCTCTAGAAATGTGGACCAAGCTAGGC 1548
 Db 68 AATAAAGAAACAGCTGTGGCTCCATTAAATACCCACACCAATGTGACCAACAGGC 9
 Qy 1549 CTCG 1552
 Db 8 CTAG 5

RESULT 13
 AAH74865/c
 ID AAH74865 standard; DNA; 5285 BP.
 XX
 AC AAH74865;
 XX
 DX 29-OCT-2001 (first entry)
 XX
 DE Nucleotide sequence of a construct comprising the PCV Rep gene.
 XX
 KW Rolling circle replication; RCR; Rep gene; gene function; Geminivirus;
 KW Circovirus; Nanovirus; gene therapy; PCV; ss.
 XX
 OS Synthetic.
 OS Porcine circovirus.
 XX
 PN W0200161024-A2.
 XX
 PD 23-AUG-2001.
 XX
 PF 15-FEB-2001; 2001WO-US005394.
 XX
 PR 16-FEB-2000; 2000US-00505477.
 XX
 PA (LARG-) LARGE SCALE BIOLOGY CORP.
 XX
 PI Palmer KE, Pogue GP;
 XX
 XX WPI; 2001-522601/57.
 DR
 XX New polynucleotide capable of rolling circle replication in host, useful
 PT for discovery of gene function, comprises Rep gene, sequences that are
 PT cis on the polynucleotide and open reading frame encoding protein of
 PT interest.
 PS
 XX Example 1; Fig 5; 6lpp; English.
 XX
 CC The specification describes a polynucleotide that is capable of rolling
 CC circle replication (RCR) in an eukaryotic host. The polynucleotide
 CC comprises a Rep gene encoding from a virus, sequences that are cis on the
 CC polynucleotide such that the Rep protein can bring about RCR of the
 CC polynucleotide, an open reading frame encoding a protein of interest
 CC capable of being expressed in the host, and optionally a multiple cloning
 CC site, where the polynucleotide lacks genes of the virus. The virus is
 CC selected from the group of genera of family Geminiviridae, Circoviridae
 CC and Nanovirus. The polynucleotide sequence is useful for the discovery of
 CC the function of genes in eukaryotic hosts, and for inducing or enhancing
 CC a trait in a host eukaryotic cell, for down-regulating a gene in a plant
 CC or in mammalian cell and thus altering or even eliminating the function
 CC of that gene, as gene sequence delivery tools for mammalian genomic
 CC approaches, for gene therapy applications (for delivering therapeutic or
 CC complementing gene products to organisms or cells), and in whole animal
 CC genomics. The present sequence represents a construct comprising the
 CC whole PCV genome. This construct contains the PCV Rep gene under the
 CC transcriptional control of its own promoter, and has the putative coat
 CC protein inactivated by insertion of the bacterial cloning vector

XX	SQ	Sequence	5285 BP; 1216 A; 1277 C; 1514 G; 1278 T; 0 U; 0 Other;
		Query Match	67.4%; Score 1195.8; DB 4; Length 5285;
		Best Local Similarity	87.7%; Pred. No. 0;
		Matches 1331; Conservative	0; Mismatches 177; Indels 9; Gaps 2;
Qy	1	GGTACCTCCGTGGATGTGTTCTCCAGCAGCTCTTCCAAATTCGAAAGTAGTAAATCCTCCGA	60
Db	1860	GGTACCTCCGTGGATGTGTTCTCCAGCAGCTCTTCCAAATTCGAAAGTAGTAAATCCTCCGA	1801
Qy	61	TAGAGAGCTTCTACAGCTGGGACAGCAGTTCGAGAGTACCATTCTCTGGGGGCGCTGATG	120
Db	1800	TAGAGAGCTTCTACAGCTGGGACAGCAGTTCGAGAGTACCATTCTCTGGGGGCGCTGATG	1741
Qy	121	CTGGTAAATCAAAATACTTCGGGGCCAAAAGGAAACAGTACCCCTCTTAGTCTCTACAGTC	180
Db	1740	CTGGTAAATCAAAATACTTCGGGGCCAAAAGGAAACAGTACCCCTCTTAGTCTCTACAGTC	1681
Qy	181	AATGGATACCGGTACACAGTCTCAGTAGATCATCTCCCAAGTAAACCAAGCCATAAAATCA	240
Db	1680	AATGGATACCGGTACACAGTCTCAGTAGATCATCTCCCAAGTAAACCAAGCCATAAAATCA	1621
Qy	241	TCCAAAACAACAACTTCTTCTCCATGATATCCATCCCAACCACTTATTTCTACTAGGCTTC	300
Db	1620	TCCAAAACAACAACTTCTTCTCCATGATATCCATCCCAACCACTTATTTCTACTAGGCTTC	1561
Qy	301	CAGTAGGTGTCCCTAGGCTCAGCAAAATTTACGGGCCCACTGGCTCTTCCCAACAACCGGGC	360
Db	1560	CAGTAGGTGTCCCTAGGCTCAGCAAAATTTACGGGCCCACTGGCTCTTCCCAACAACCGGGC	1501
Qy	361	GGGCCCACTATGACGTGTACAGCTGTCTTCCAATCAGCTCTCTGCATCTTTCGCGCTCACT	420
Db	1500	GGGCCCACTATGACGTGTACAGCTGTCTTCCAATCAGCTCTCTGCATCTTTCGCGCTCACT	1441
Qy	421	TTCAAAAGTTCAGCCAGCCCGGGAAATTTCTCATACAGTTACAGGAACTGCTCGGCT	480
Db	1440	TTCAAAAGTTCAGCCAGCCCGGGAAATTTCTCATACAGTTACAGGAACTGCTCGGCT	1381
Qy	481	ACAGTCACAAAGACCCCGTCTCCAAAGGGTACTTCACAGCAGTAGACAGTCTGCTGCGC	540
Db	1380	ACAGTCACAAAGACCCCGTCTCCAAAGGGTACTTCACAGCAGTAGACAGTCTGCTGCGC	1321
Qy	541	TTCCCTCGTTTCCGGAGCTCCACACTCGATAAGTATGTGGCTCTTTTACTCGAGTAT	600
Db	1320	TTCCCTCGTTTCCGGAGCTCCACACTCGATAAGTATGTGGCTCTTTTACTCGAGTAT	1261
Qy	601	TCCTTATTCGCTGGTTCGTTTCTTTCGTTTCTCGATGTGGCAGCGGGACCAAAATAC	660
Db	1260	TCCTTATTCGCTGGTTCGTTTCTTTCGTTTCTCGATGTGGCAGCGGGACCAAAATAC	1201
Qy	661	CACCTTCACCTTGTTAAAGTCGTCTTTAGCAAAATTCGCAAAACCCCTGGAGGTGAGGA	720
Db	1200	CACCTTCACCTTGTTAAAGTCGTCTTTAGCAAAATTCGCAAAACCCCTGGAGGTGAGGA	1141
Qy	721	GTTCTACCTCTTCCAAACCTTCTCTCGCACAAAATAATCAAAAGGAGGATTTGGA	780
Db	1140	GTTCTACCTCTTCCAAACCTTCTCTCGCACAAAATAATCAAAAGGAGGATTTGGA	1081
Qy	781	AGCTCCCGATTTTGTGTTTTTCTCTCTCGGAAGAATTAAAGGGTGGAACCCACCTC	840
Db	1080	AGCTCCCGATTTTGTGTTTTTCTCTCTCGGAAGAATTAAAGGGTGGAACCCACCTC	1021
Qy	841	TTATGGGGTTCGGGGCGCTTTTCTTGCTTGGCAATTTTCACTGACGCTCCGAGGTGCTG	900
Db	1020	TTATGGGGTTCGGGGCGCTTTTCTTGCTTGGCAATTTTCACTGACGCTCCGAGGTGCTG	961
Qy	901	CCGCTGCGAAGTCGGCTGGTAAATACACAGCAGCGCACTTCTTTTCACTTTTATAGGATG	960
Db	960	CCGCTGCGAAGTCGGCTGGTAAATACACAGCAGCGCACTTCTTTTCACTTTTATAGGATG	901
Qy	961	ACGTATCCAGGAGCGGTTACCGCAGAGAAGACACCGCCCGCCGACGCACTTTTGGCCAG	1020

Db	900	ACGTGGCCAGGAGGCGTTACCGCAGAGAGAGACCGCGCCCGCGACCCATCTTGGAAAC	841
Qy	1021	ATCCTCCGCGCGCGCCCTCGCTCGTCCACCC-----CGCCACCGCTACCGTTGGAGA	1074
Db	840	ATCCTCGGAGAGACCATATTTGGCAGACCCCGCCTTCAGAAACCGTTACAGATGCGCG	781
Qy	1075	AGGAAATATGGCATCTTCAACACCGCGCTCTCCGCACTTCGGATATATCTGTCAAGGCT	1134
Db	780	CGAAGACGGGTATCTTCAATTCGCCGCTTTCTACAGAAATTTGTACTCAACATAAAGGA	721
Qy	1135	ACCACAGTCAGAACGCCCTCCTCGGCGGTGGACATGATGAGATTTAATATTGACGACTTT	1194
Db	720	G---GATATCGCAGCCATCTTGAATGTTAACTACTCAATTCACATCGGCCAGTTC	664
Qy	1195	GTTCCTCCCGGAGGGGACCAACAAATCTTATACCTTTTGAATACTACAGAATAAGA	1254
Db	663	CTCCCCCTCAGCGGCGACCAACCCCTACCCCTTTCCTTCCCACTACCGTATTAGA	604
Qy	1255	AAGGTTAAGTTGAATTTCTGGGCCCTGTCTCCCCCATCACCCAGGCGTATAGGGAGTGGCG	1314
Db	603	AAGGCTAAATATGAATTTTACCCCGAGAGACCCCATCACCTCTTAATCAAAGAGGTGTGGG	544
Qy	1315	TCCACTGCTGTATTCTTAGATGATAAATTGTGTAAAGGCGCACAGCCCTTAACCTATGAC	1374
Db	543	TCCACTGTTGTATTCTTGGATGCCAATTGTAAACCCCTTCCACCAACTTGGCCTATGAC	484
Qy	1375	CCATATGAACTACTCTCTCCGCCATACAAATCCCCCAACCCCTTCTCTACCACTCCCGT	1434
Db	483	CCCTATTATTAACTACTCTCTCCGCCACACATTAAGGCGCCCTTTACCTACCACTCCAGG	424
Qy	1435	TACTTCACACCCAAACCTGTTCTTGATCTCCACCATTTGATTACTTCCAAACCAATAACAA	1494
Db	423	TACTTCACCCCAAACTGAGCTGGACCAACAAATTTGATTGGTTTCCACCCCAATAATAA	364
Qy	1495	AGGAATCAGCTTTGGAT	1511
Db	363	AGAAACCACTGTGGCT	347
RESULT 14			
ID	ABX94355/c		
XX	ID ABX94355 standard; DNA; 5285 BP.		
XX	AC ABX94355;		
XX	19-JUN-2003 (first entry)		
XX	Rolling circle replicon construct 1.		
DE	Virucide; vaccine; gene therapy; Rep gene; rolling circle replication;		
KW	Construct 1; PCV; ds.		
XX	OS Porcine circovirus.		
OS	Simian virus 40.		
XX	OS Synthetic.		
XX	US2002187952-A1.		
EN	12-DEC-2002.		
XX	20-DEC-2001; 2001US-00038001.		
FD	16-FEB-2000; 2000US-00505477.		
XX	(PALM/) PALMER K E.		
PA	(POGU/) POGUE G G.		
PA	(MCCO/) MCCORMICK A.		
XX	Palmer KE, Pogue GG, McCormick A;		
PI	WPI; 2003-341042/32.		
XX	New rolling circle DNA replicons or polynucleotides, useful in vaccine or		
XX	XT		

New rolling circle DNA replicons or polynucleotides, useful in vaccine or

gene therapy applications, for eliciting an immunization reaction in a eukaryotic host, or for inducing or enhancing a function or trait in a host eukaryotic cell.

Example 1; Fig 5; S1pp; English.

The invention relates to a polynucleotide capable of eliciting an immunisation reaction in a eukaryotic host to a peptide or polypeptide. The polynucleotide encodes the peptide or polypeptide, and contains elements of a viral genome (i.e. the Rep gene) that is capable of rolling circle replication. The peptide or polypeptide is capable of expression in the eukaryotic host. Also included are constructing a polynucleotide capable of eliciting an immunisation reaction in a host (comprising inserting a sequence encoding a peptide or polypeptide into the polynucleotide, where the polynucleotide comprises elements of a viral genome that is capable of rolling circle replication) and immunising a host comprising administering a composition comprising the polynucleotide into the host. Substantially higher levels of Igg antibody induction were seen in mice injected with immunogenic protein insert linked to a rolling circle replication cassette versus immunogenic protein inserted into a non-rolling circle replicon mammalian expression vector. Levels of Igg antibody through successive bleeds were higher for both luciferase and beta-galactosidase expression cassettes linked to a porcine Circovirus cassette, as compared to non-rolling circle replicon linked vectors or injection with saline alone, vector without insert, purified luciferase or beta-galactosidase. The polynucleotide capable of rolling circle replication in a eukaryotic host is useful in vaccine or gene therapy applications, or for eliciting an immunisation reaction in a eukaryotic host. The rolling circle replicons or polynucleotides are also useful for the discovery of the function of genes in eukaryotic hosts, for inducing or enhancing a function or trait in a host eukaryotic cell, or for down-regulating a gene in a plant or mammalian cells, which alters or even eliminates the function of that gene. The ancillary protein is useful for potentiating an immunisation reaction in the host elicited by the peptide or polypeptide. The present sequence (termed Construct 1) is a polynucleotide of the invention comprising the whole PCV (porcine circovirus) cloned into the Invitrogen cloning vector pCR BLUNT II-TOPO. The PCV Rep gene is under control of its own promoter and the coat protein gene is inactivated by insertion of the vector

Sequence 5285 BP; 1216 A; 1276 C; 1515 G; 1278 T; 0 U; 0 Other;

Query Match 67.4%; Score 1195.8; DB 8; Length 5285;
 Best Local Similarity 87.7%; Pred. No. 0;
 Matches 1331; Conservative 0; Mismatches 177; Indels 9; Gaps 2;

1 GGTACCTCCGCGGATTTCTCCAGCAGTCTTCCAAAATTCGAAAGTAGTAATCTCCGA 60
 1860 GGTACCTCCGCGGATTTCTCCAGCAGTCTTCCAAAATTCGAAAGTAGTAATCTCCGA 1801

61 TAGAGAGCTTCTACAGCTGGGACAGAGTTGAGAGTACCATTTCTGGGGGCTGATTG 120
 1800 TAGAGAGCTTCTACAGCTGGGACAGAGTTGAGAGTACCATTTCTGGGGGCTGATTG 1741

121 CTGGTAATCAAAATACATCTCGCGGCCCCAAAAGGAAACAGTACCCCTTTAGTCTCTACAGTC 180
 1740 CTGGTAATCAAAATACATCTCGCGGCCCCAAAAGGAAACAGTACCCCTTTAGTCTCTACAGTC 1681

181 AATGGATACCGGTACACAGTCTCAGTAGATCATCCCAAGGTAAACAGCCATAAAATCA 240
 1680 AATGGATACCGGTACACAGTCTCAGTAGATCATCCCAAGGTAAACAGCCATAAAATCA 1621

241 TCCAAAACAACTCTCTCCATGATATCCATCCACCACTTATTTCTACTAGGCTTC 300
 1620 TCCAAAACAACTCTCTCCATGATATCCATCCCAAGGTAAACAGCCATAAAATCA 1561

301 CAGTAGGTGTCCTTAGGCTCAGCAAAATTAAGGGCCCACTGGCTCTTCCCAACACCGGGC 360
 1560 CAGTAGGTGTCCTTAGGCTCAGCAAAATTAAGGGCCCACTGGCTCTTCCCAACACCGGGC 1501

361 GGGCCCACTATGACGTGTACAGTGTCTTCCAAATCAAGCTGTGCTGCTCCCGCTCACT 420
 1500 GGGCCCACTATGACGTGTACAGTGTCTTCCAAATCAAGCTGTGCTGCTGCTCCCGCTCACT 1441

Qy 421 TTCAAAGTTTCAGCCAGCCCGCGGAAATTTCTCACATACGTTTACAGGAACTGCTCGGCT 480
 Db 1440 TTCAAAGTTTCAGCCAGCCCGCGGAAATTTCTCACATACGTTTACAGGAACTGCTCGGCT 1381

Qy 481 ACAGTCACCAAGACCCCGCTCTCCAAAAGGGTACTCACAGCAGTAGACAGGTGCTGCGC 540
 Db 1380 ACAGTCACCAAGACCCCGCTCTCCAAAAGGGTACTCACAGCAGTAGACAGGTGCTGCGC 1321

Qy 541 TTCCCTGTTTCGCGGAGCTCCACTCGATAAGTATGTGGCTTCTTTTACTGCAGTAT 600
 Db 1320 TTCCCTGTTTCGCGGAGCTCCACTCGATAAGTATGTGGCTTCTTTTACTGCAGTAT 1261

Qy 601 TCTTTATCTGCTGCTGCTGCTTCTTCTCGATGTCGAGGGGACCAAAATAC 660
 Db 1260 TCTTTATCTGCTGCTGCTGCTTCTTCTCGATGTCGAGGGGACCAAAATAC 1201

Qy 661 CACTTCACTTGTAAAGTCTGCTTCTTTAGCAAAATTCGCAAAACCCCTCGAGGTGAGGA 720
 Db 1200 CACTTCACTTGTAAAGTCTGCTTCTTTAGCAAAATTCGCAAAACCCCTCGAGGTGAGGA 1141

Qy 721 GTTCTACCTTTCGCAACCTTCTCGCCACCAAAATAATCAAAAAGGGAGATGGA 780
 Db 1140 GTTCTACCTTTCGCAACCTTCTCGCCACCAAAATAATCAAAAAGGGAGATGGA 1081

Qy 781 AGCTCCGCTATTTTGTCTCTCTCGAAAGGATTTAAGGGTGAACACCCACCTC 840
 Db 1080 AGCTCCGCTATTTTGTCTCTCTCGAAAGGATTTAAGGGTGAACACCCACCTC 1021

Qy 841 TTAAGGGTTGCGGGCGCTTTTCTTCTGTTGGCATTTTCACTCACTGCGTGGAGGTGCTG 900
 Db 1020 TTAAGGGTTGCGGGCGCTTTTCTTCTGTTGGCATTTTCACTCACTGCGTGGAGGTGCTG 961

Qy 901 CCCTGCGGAGTGGCTGTGTAATCTACAGAGCGCACTTCTTCACTTTTATAGATG 960
 Db 960 CCCTGCGGAGTGGCTGTGTAATCTACAGAGCGCACTTCTTCACTTTTATAGATG 901

Qy 961 ACCTATCTCAAGAGGGCTTACCGCAGAAAGACACCGCCCCCGCAGCCATCTTTGGCCAG 1020
 Db 900 ACCTATCTCAAGAGGGCTTACCGCAGAAAGACACCGCCCCCGCAGCCATCTTTGGAAAC 841

Qy 1021 ATCTCCGCGCGCCCGCTGGCTGCTGCCACCC-----CGCCACCGCTACCGTTGAGGA 1074
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Qy 1075 AGGAAAATGGCATCTTCAACACCGCTCTCCGCGACCTTCGATATACGTCAAGSCT 1134
 Db 780 CGAAAGACGGGTATCTCAATTTCCGCTTTTCTAGAGATTTGTACTCACCATAAAGGA 721

Qy 1135 ACCACAGTCAGAACCGCTCTCTGGGGGTGGACATGATGAGATTTAATATTGACGACTTT 1194
 Db 720 G---GATACTCGCAGCCATCTTGGATGTTAACTACTCTCAATTCACATCGGCCAGTTC 664

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 Db 664 CTCCCGCTCTCAGCGGACCAACCCCTACCTTTTCCAATACTACCGTATTAGA 604

Qy 1255 AAGGTTAAGTTCAATTTCTGGCCCTGCTCCCGCATCACCCAGGGTGATAGGGAGTGGGC 1314
 Db 604 AAGGTTAAGTTCAATTTTACCCGAGAGACCCCATCACTCTTAATCAAGAGGTGTTGGG 544

Qy 1315 TCCACTGCTGTTATTTCTAGATGATACTTTGTAAAGGCGCCACAGCCCTTAACCTATGAC 1374
 Db 544 TCCACTGCTGTTATTTCTGGATGCCAATTTGTAAACCCCTCCACCACTTTGGCCTATGAC 484

Qy 1375 CCATATGATAACTTCTCTCCCGCATCAATCCCCCAACCCCTTCTCTACGACTCCCGT 1434
 Db 484 CCCTATATTAACCTACTCTCTCCCGCATCAATCAAGGAGCGCCCTTTTACTTCACTCCAGG 424

Qy 1435 TACTTCAACCCCAAACTGTTCTTGTACTCCACCATTTGATTACTTCCAAACCAATAACAA 1494
 Db 424 TACTTCAACCCCAAACTGTTCTTGTACTCCACCATTTGATTACTTCCAAACCAATAACAA 364

Qy	1135	ACCACAGTCAGAACGCCCTCTCTGGCGGTGGACATGATGAGATTTAATATTGACGACTTT	1194
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Qy	1195	GTTCCCCCGGAGGGGGACCAACAAATCTCTATACCCCTTTGAATACTACAGAAATAAGA	1254
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Qy	1255	AAGGTTAAGGTTGAATTTCTGGCCCTGCTCCGCCATCACCCAGGGGTGATAGGGGAGTGGC	1314
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Qy	1315	TCCACTGCTGTATTCTAGATGATACTTTGTAAAGGCCACAGCCCTTAACCTATGAC	1374
Db	356	TCCACTGTTGTTATCTTGGATGCCAATTTGTAAACCCCTCCACCAACTTGGCCTATGAC	297
Qy	1375	CCATATGTAAACTACTCCTCCCGCCATACAAATCCCCCAACCCCTTCTCCTACCACTCCCGT	1434
Db	296	CCCTATATTAACTACTCCTCCCGCCACACCAATAAGGCAGGCCCTTTACCTACCACCTCCAGG	237
Qy	1435	TACTTCACACCCAAACCTGTTCTTGACTCCACCATTGATTACTTCCAAACCAATACAAA	1494
Db	236	TACTTCACCCCAACCTGAGCTGGACCAACAAATTGATTGGTTCCACCCCAATATAAA	177
Qy	1495	AGGAATCAGCTTTGGAT	1511
Db	176	AGAACCCAGCTGTGGCT	160

Search completed: August 5, 2005, 02:42:15
Job time : 987 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 4, 2005, 23:27:58 ; Search time 7724 Seconds
(without alignments)

11122.618 Million cell updates/sec

Title: US-10-808-964A-2

Perfect score: 1773

Sequence: 1 ggtactctcggtgattgttc.....caaatcggttcgggtacc 1773

Scoring table:

IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: gb.ba.*
2: gb.htg.*
3: gb.in.*
4: gb.om.*
5: gb.ov.*
6: gb.pat.*
7: gb.ph.*
8: gb.pl.*
9: gb.pr.*
10: gb.ro.*
11: gb.sta.*
12: gb.sv.*
13: gb.un.*
14: gb.vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 1	1386.4	78.2	1768	14 AF264042	AF264042 Porcine c
C 2	1378.4	77.7	1768	14 AF264040	AF264040 Porcine c
C 3	1370.4	77.3	1768	14 AF264039	AF264039 Porcine c
C 4	1370.4	77.3	1768	14 AF520783	AF520783 Porcine c
C 5	1370.4	77.3	1768	14 AF544024	AF544024 Porcine c
C 6	1368.8	77.2	1768	14 AF264041	AF264041 Porcine c
C 7	1367.2	77.1	1768	14 AF264038	AF264038 Porcine c
C 8	1364	76.9	1768	14 AF264043	AF264043 Porcine c
C 9	1364	76.9	1768	14 AF454546	AF454546 Porcine c
C 10	1357.6	76.6	1768	14 AF201309	AF201309 Porcine c
C 11	1346.4	75.9	1768	14 AF201305	AF201305 Porcine c
C 12	1346.4	75.9	1768	14 AF201308	AF201308 Porcine c
C 13	1343.2	75.8	1768	14 AF201306	AF201306 Porcine c
C 14	1341.6	75.7	1768	14 AF201310	AF201310 Porcine c
C 15	1340	75.6	1768	14 AF201307	AF201307 Porcine c
C 16	1306	73.7	1767	12 AJ623306	AJ623306 Synthetic
C 17	1304.4	73.6	1767	14 AF201311	AF201311 Porcine c
C 18	1303.4	73.5	1767	14 AF122275	AF122275 Porcine c
C 19	1301.2	73.4	1767	14 AY288134	AY288134 Porcine c

C 20	1296.4	73.1	1767	14 AY294310	AY294310 Porcine c
C 21	1288.4	72.7	1767	14 AY288133	AY288133 Porcine c
C 22	1285.2	72.5	1768	6 AX379562	AX379562 Sequence
C 23	1285.2	72.5	1768	14 AY099498	AY099498 Porcine c
C 24	1278.8	72.1	1768	6 AX379560	AX379560 Sequence
C 25	1278.8	72.1	1768	14 AY099496	AY099496 Porcine c
C 26	1277.2	72.0	1768	6 AX379564	AX379564 Sequence
C 27	1277.2	72.0	1768	14 AY099500	AY099500 Porcine c
C 28	1274	71.9	1768	6 AX379561	AX379561 Sequence
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C 30	1274	71.9	1768	14 AY099495	AY099495 Porcine c
C 31	1274	71.9	1768	14 AY099499	AY099499 Porcine c
C 32	1262.6	71.2	1759	14 PCCOMGEN	Y09921 Porcine chr
C 33	1261.4	71.1	1768	14 AF305532	AF305532 Porcine c
C 34	1261.4	71.1	1768	14 AF305533	AF305533 Porcine c
C 35	1252	70.6	1762	6 AX379559	AX379559 Sequence
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C 37	1218.2	68.7	1759	6 AX379565	AX379565 Sequence
C 38	1218.2	68.7	1759	14 AY099501	AY099501 Porcine c
C 39	1196.8	67.5	7400	6 AX226286	AX226286 Sequence
C 40	1195.8	67.4	5225	6 AX226280	AX226280 Sequence
C 41	1195.8	67.4	5650	6 AX226281	AX226281 Sequence
C 42	1059.8	59.8	1759	6 A97282	A97282 Sequence 5
C 43	1059.8	59.8	1759	6 AR145612	AR145612 Sequence
C 44	1059.8	59.8	1759	6 CQ768117	CQ768117 Sequence
C 45	1059.8	59.8	1759	6 AR204537	AR204537 Sequence

ALIGNMENTS

RESULT 1
AF264042/c
LOCUS Porcine circovirus type 2 isolate 40895 complete genome.
DEFINITION Porcine circovirus type 2 isolate 40895 complete genome.
ACCESSION AF264042
VERSION AF264042.1 GI:9392644
SOURCE Porcine circovirus 2
ORGANISM Porcine circovirus 2
KEYWORDS Viruses; ssDNA viruses; Circoviridae; Circovirus.
REFERENCE 1 (bases 1 to 1768)
AUTHORS Fenaux,M., Halbur,P.G., Gill,M., Toth,T.E. and Meng,X.J.
TITLE Genetic characterization of type 2 porcine circovirus (PCV-2) from pigs with postweaning multisystemic wasting syndrome in different geographic regions of North America and development of a differential PCR-restriction fragment length polymorphism assay to detect and differentiate between infections with PCV-1 and PCV-2
JOURNAL J. Clin. Microbiol. 38 (7), 2494-2503 (2000)
MEDLINE 20341537
PUBMED 10878032
REFERENCE 2 (bases 1 to 1768)
AUTHORS Fenaux,M., Halbur,P.G., Gill,M., Toth,T.E. and Meng,X.J.
TITLE Direct Submission
JOURNAL Submitted (08-MAY-2000) VMRCVM, Virginia Tech, 1410 Prices Fork Road, Blacksburg, VA 24061, USA
FEATURES
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ORIGIN

Query Match	78.2%;	Score 1386.4;	DB 14;	Length 1768;
Best Local Similarity	90.3%;	Pred. No. 0;		
Matches 1543;	Conservative 0;	Mismatches 146;	Indels 19;	Gaps 5;
QY	3	TACCTCCGTGGATTGTTCTCCAGCAGTCTTCCAAAATTGCAAGTAGTAATCCTCCGATA	62	
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QY	63	GAGAGCTTCTACAGCTGGGACAGCAGTGTGAGGAGTACCATTCTCTGGGGGGCTGATGCT	122	
Db	1643	GAGAGCTTCTACAGCTGGGACAGCAGTGTGAGGAGTACCATTCCAAACGGGGTCTGATGCT	1584	
QY	123	GGAATACAAATACGTGCGGGCCAAAAGGAACAGTACCCCTTTAGTCTCTACAGTCAA	182	
Db	1583	GGAATACGAATACGTGCGGGCCAAAAGGTAACGTTCCACCTTTAGTCTCTACAGTCAA	1524	
QY	183	TGATACCGGTACACAGTCTCAGTAGATCATCCCAAGTAAACAGCAGCCATAAAATCATC	242	
Db	1523	TGATATCGATCACAGTCTCAGTAGATCATCCCAAGCAGCCATAAAAGTCAATC	1464	
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QY	363	GCCCACTATGAGGTGTACAGTGTCTTCCAATCAGCTGTGCTGCATCTTCCCGCTCACTTT	422	
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QY	423	CAAAAGTTTCAGCCAGCCCGCGGAAATTTCTCATAGTTACAGGAAACTGCTCGGGTAC	482	
Db	1283	CAAAAGTTTCAGCCAGCCCGCGGAAATTTCTGACAAACAGTTTACAGGCTGTGCTCTGCAAC	1224	
QY	483	AGTACCAAGAACCCCGTCTCAAAGGCTACTCAGCAGTAGACAGGTGCTCGGCTT	542	
Db	1223	GGTACCAAGAACCCCGTCTCAAAGGCTACTCAGCAGTAGACAGGTGCTGCTCGGCTT	1164	
QY	543	CCCTGTGTTCCGGGAGCTCCACACTCGATAAGTATGTGGCCCTTCTTACTCAGTATTC	602	
Db	1163	TCTTTGAGATCAGGAGCTCCACATTCATAGTAAGTTGCTTCTTACTCAGTATTC	1104	
QY	603	TTTATTTCTGCTGGTTCGTTTCTTCTGTTTCTCGATGTGGCAGCGGGCCAAAATACCA	662	
Db	1103	TTTATTTCTGCTGATCAGTTCCTTTGGCTTCTCGATATGGCAGCGGGCCAAAATACCA	1044	
QY	663	CTTCACTTGTAAAGTCTGCTTCTTAGCAAAATTCGCAAAACCCCTGGAGGTGAGGAGT	722	
Db	1043	CTTCACTTGTAAAGTCTGCTTCTTCTTCAAAATTTAGCAAAACCCCTGGAGGTGAGGAGT	984	
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QY	843	ATGGGGTTGGGGCGGCTT-----TTCTTCTTGGGCAATTTT-----CACTGACGCTG	889	
Db	863	ATGTGGTTGGGTCGCTTCTTCCATTTCTTCTTGGGCATGTTGCTGCTGAGGTGCTG	804	
QY	890	CCGAGGTGCTGCGCTGCGCGAAGTGCCTGTGTAATACTACACAGCGCACCTTCTTCACT	949	
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Db	506	ACTTTGTTCCCGGGAGGGGGACCAACAAAATCTCTATACCTTTTGAATACTACAGAA	447	
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Db	446	TAAGAAAGGTTAAGTTGAATTTCTGGCCCTGCTCCCCCATCACCAGGGTGATAGGGAG	387	
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Db	386	TGGGCTCCAGTCTGTTATTTCTAGATGATTAATTTGTAAACAAAGGCCACAGCCCTAACCT	327	
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RESULT 2
AF264040/c
LOCUS AF264040
DEFINITION Porcine circovirus type 2 isolate 10489 complete genome.
ACCESSION AF264040

VERSION	AF264040.1	GI:9392638	
KEYWORDS	Porcine circovirus 2		
SOURCE	Porcine circovirus 2		
ORGANISM	Viruses; ssDNA viruses; Circoviridae; Circovirus.		
REFERENCE	1 (bases 1 to 1768)		
AUTHORS	Fenaux,M., Halbur,P.G., Gill,M., Toth,T.E. and Meng,X.J.		
TITLE	Genetic characterization of type 2 porcine circovirus (PCV-2) from pigs with postweaning multisystemic wasting syndrome in different geographic regions of North America and development of a differential PCR-restriction fragment length polymorphism assay to detect and differentiate between infections with PCV-1 and PCV-2		
JOURNAL	J. Clin. Microbiol. 38 (7), 2494-2503 (2000)		
MEDLINE	20341537		
PUBMED	10878032		
REFERENCE	2 (bases 1 to 1768)		
AUTHORS	Fenaux,M., Halbur,P.G., Gill,M., Toth,T.E. and Meng,X.J.		
TITLE	Direct Submission		
JOURNAL	Submitted (08-MAY-2000) VMRCVM, Virginia Tech, 1410 Prices Fork Road, Blacksburg, VA 24061, USA		
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QY	63	GAGAGCTTCTACAGCTGGGACAGCAGTTCGAGAGTACCATTCCTGGGGGCGCTGATTGCT	122
Db	1643	GAGAGCTTCTACAGCTGGGACAGCAGTTCGAGAGTACCATTCGAAACGCGGCTGATTGCT	1584
QY	123	GGAATCAAAATACCTGCGGGCCAAAGGAAACAGTACCCCTTTTAGTCTCTACAGTCAA	182
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QY	483	AGTCAACCAAGACCCCGTCTCCAAAGGGTACTCAGCAGTAGACAGGTCTGCTGCGCTT	542
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QY	603	TTTATTTCTGCTGCTGCTGCTTCTTCTGATGTTGGCAGCGGACCAAAATACCA	662
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QY	723	TCTACCTCTTCCAAACCTTCTCCGCAAAACAAATAATCAAAAGGAGATTGGAAG	782
Db	983	TCGTCTTCTCTCATACCTCTCTCCCAACAAATAAAATAATCAAAATAGGAGATTGGGAG	924
QY	783	CTCCGATTTTGTGTTTCTCTCTCGAAGGATTTTAAAGGTGAACACCCACCTCTT	842
Db	923	CTCCGATTTTCTTGGCTGCTCTTGGAGGATTTTACGCGTGAACACCCACCTTT	864
QY	843	ATGGGTTTGGCGCGCTT-----TTCTTGTCTGGCATTTT-----CACTGACGCTG	889
Db	863	ATGTGTTGGGTCCGCTTCTTCCATTTCTTCTGCTGGCATGTTGCTGAGGTGCTG	804
QY	890	CCGAGGTGCTGCGCTGCGAAGTGGCTGTAATACTACAGCAGGCACTTCTTTCACT	949
Db	803	CCGAGGTGCTGCGCTGCGAAGTGGCTGTAATACT--TACAGCGCACTTCTTTCTGTT	746
QY	950	TTTATAGATGAGTATCCAGGAGGCTTACCGCAGAGAGACACCGCCCCCGCAGCC	1009
Db	745	TTCA--GCTATGACGTATCCAGAGGCGTTCACCGCAGAGAGACACCGCCCCCGCAGCC	687
QY	1010	ATCTTGGCCAGATCTCCGCGCGCCCTCTGCTGCTGCTCCACCCCGCCACCGCTACCGTT	1069
Db	686	ATCTTGGCCAGATCTCCGCGCGCCCTCTGCTGCTCCACCCCGCCACCGCTACCGTT	627
QY	1070	GGAGAGGAAATATGGCATCTTCAACACCGCTCTCCCGCACCTTCGGATATATCTGCA	1129
Db	626	GGAGAGGAAATATGGCATCTTCAACACCGCTCTCCCGCACCTTCGGATATATCTGTA	567
QY	1130	AGGCTACCAAGTACAGAGCGCTCTCGGGGTGAGCATGATGATGATTAATATTGACG	1189
Db	566	AGGCTACCAAGTACAGAGCGCTCTCGGGGTGAGCATGATGATGATTAATATTGACG	507
QY	1190	ACTTTGTTTCCCCCGGAGGGGAGCAACAAATCTCTATACCTTTTGAATACTACAGAA	1249
Db	506	ACTTTGTTTCCCCCGGAGGGGAGCAACAAATCTCTATACCTTTTGAATACTACAGAA	447
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QY TCGGCACTGCTCGAAACAGTATATACGACAGGCTACAATATCGTGTACCACTGT 1609
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RESULT 3
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LOCUS Porcine circovirus type 2 isolate 26607 complete genome. 1768 bp DNA linear VRL 23-JUL-2000
DEFINITION Porcine circovirus type 2 isolate 26607 complete genome.
ACCESSION AF264039
VERSION AF264039.1 GI:9392635
KEYWORDS
SOURCE Porcine circovirus 2
ORGANISM Porcine circovirus 2
REFERENCE 1 (bases 1 to 1768)
Virus; ssDNA viruses; Circoviridae; Circovirus.
Fenaux,M., Halbur P.G., Gill,M., Toth,T.E. and Meng,X.J.
TITLE Genetic characterization of type 2 porcine circovirus (PCV-2) from pigs with postweaning multisystemic wasting syndrome in different geographic regions of North America and development of a differential PCR-restriction fragment length polymorphism assay to detect and differentiate between infections with PCV-1 and PCV-2
J. Clin. Microbiol. 38 (7), 2494-2503 (2000)
JOURNAL 20341537
MEDLINE
PUBMED 10878032
REFERENCE 2 (bases 1 to 1768)
Fenaux,M., Halbur,P.G., Gill,M., Toth,T.E. and Meng,X.J.
AUTHORS Direct Submission
TITLE Submitted (08-MAY-2000) VMRCVM, Virginia Tech, 1410 Prices Fork Road, Blacksburg, VA 24061, USA
JOURNAL Location/Qualifiers
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Best Local Similarity 89.8%; Pred. No. 0;
Matches 1533; Conservative 0; Mismatches 156; Indels 19; Gaps 5;
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QY 303 GTAGGTGCTTCCAGCTCAGCAAAATACGGGGCCCACTGGCTCTTCCACAAACCGGGCG 362
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QY 423 CAAAGTTTCCAGCAGCCCGCGGAAATTTCTCACAATAGCTTACAGGAAATCTGCTCGGTAC 482
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QY	783	CTCCCGTATTTGTTTCTCTCTCTCGGAAGGATTTAAGGTGCAACACCACTCTT	842
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Db	863	ATGTTGTTGGGTGCGCTTCTTCCATTTCTTCTGTCGGCATGTTGCTCTGAGGTGCTG	804
QY	890	CCGAGTGTGCGCTGCGGTCGCAAGTGTGCTGTAATACTACAGAGCGCATCTTTTCACT	949
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QY	950	TTTATAGGATGAGTATCCAAAGGCGGTTACGCGAGAGAGACACCGCCCGCCGAGCC	1009
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QY	1010	ATCTTGGGCAGATCTCTCGCCCGCGCCCTGCTGCTCCACCGCCCGCCACCGCTACCGTT	1069
Db	686	ATCTTGGGCAGATCTCTCGCCCGCGCCCTGCTGCTCCACCGCCCGCCACCGCTACCGTT	627
QY	1070	GGAGAAGGAAAATGGCATCTTTCAACACCGGCTCTCTCCGCACTTTCGGATATATGTCA	1129
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QY	1130	AGGCTACCACTGAGAGCGGCTCTCTGGCGGTGAGATGATGATTTATATTTGAGG	1189
Db	566	AGCGTACCACTGAGAGCGGCTCTCTGGCGGTGAGATGATGATTTATTAACCTTTGAGG	507
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Db	506	ACTTTTGTCCCGGAGGGGAGCAACAAATCTCTATACCTTTGAATACTACAGAA	447
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Db	446	TAAAGAAAGTTAAGTTGAATTTCTGCGCTCTCTCCCGCATCACCGAGGTGATAGGGAG	387
QY	1310	TGGGCTCCACTGCTGTTATCTAGATGATTAATTTGTAACAGGCGCACGCGCTTAACCT	1369
Db	386	TGGGCTCCACTGCTGTTATCTAGATGATTAATTTGTAACAGGCGCACGCGCTTAACCT	327
QY	1370	ATGACCCATATGTAATACTACTCTCCCGCATACAAATCCCAACCTTCTCTACCACT	1429
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QY	1550	TGGGCACTGCGTTTCAAAACAGTATATACGACGAGCTTACAAATATCGTGTAAACATGT	1609
Db	146	TGGGCACTGCGTTTCAAAACAGTATATACGACGAGCTTACAAATATCGTGTAAACATGT	87
QY	1610	ATGTACAATTACAGAAATTTAATCTTAAAGACCCCACTTAAACCTTAAATGAATAAAA	1669
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RESULT 4			
AF520783/c			
LOCUS			
1768 bp DNA linear VRL 08-JUL-2002			

DEFINITION	Porcine circovirus type 2 isolate JHP, complete genome.		
ACCESSION	AF520783		
VERSION	AF520783.1 GI:21702689		
KEYWORDS	Porcine circovirus 2		
SOURCE	Porcine circovirus 2		
ORGANISM	Viruses; ssDNA viruses; Circoviridae; Circovirus.		
REFERENCE	1 (bases 1 to 1768)		
AUTHORS	Park,J.H., Roh,I.S., Song,J.Y., Cha,S.H. and Choi,E.J.		
TITLE	Direct Submission		
JOURNAL	Submitted (07-JUN-2002) Virology Division, National Veterinary Research and Quarantine Service, Anyang 6-Dong, Anyang, Gyeonggi 430-824, Korea		
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Query Match	77.3%;	Score 1370.4;	DB 14; Length 1768;
Best Local Similarity	89.8%;	Pred. No. 0;	
Matches 1533; Conservative	0;	Mismatches 156;	Indels 19; Gaps 5;
Qy	3	TACCTCCGTGGATTGTTCTCCAGCAGTCTTCCAAAATTGCAAGTAGTAATCCTCCGATA	62
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Qy	63	GAGAGCTTCTACAGCTGGGACAGCAGTTCAGGAGTAGCAATTCCTGGGGGCTGATTGCT	122
Db	1643	GAGAGCTTCTACAGCTGGGACAGCAGTTCAGGAGTAGCAATTCCAACCGGGCTCGATTGCT	1584
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Db	1583	GGTAATCAGAAATACTCGGGGCCAAAAGGATACAGTTCACCTTTGGTCTCTACAGTCAA	1524
Qy	183	TGGATACCGGTCAACAGTCTCAGTAGATCATCCCAAGGTAAACAGCCATAAATAATCATC	242
Db	1523	TGGATATCGATCACAGCTCTCAGTAGATCATCCCAAGGTAAACAGCCATAAATAATCATC	1464
Qy	243	CAAAACAACAACTTCTTCCATGATATCCATCCCAACCACTTATTCTACTAGGCTTCCA	302
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Qy	303	GTAGGTGCTCCCTAGGCTCAGCAAAATTAAGGGCCCACTGGCTCTTCCCAACACCGGGCG	362
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LOCUS Porcine circovirus type 2 strain KSY-2 from Korea, complete genome.
DEFINITION
ACCESSION AF544024
VERSION AF544024.1 GI:23267184
KEYWORDS
SOURCE Porcine circovirus 2
ORGANISM Porcine circovirus 2
VIRUSES; ssDNA viruses; Circoviridae; Circovirus.
REFERENCE 1 (bases 1 to 1768)
AUTHORS Kim, K.M., Song, Y.K., Park, H.S. and Kang, S.Y.
TITLE Characterization of porcine circovirus type 2 isolated in Korea
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1768)
AUTHORS Kim, K.M., Song, Y.K., Park, H.S. and Kang, S.Y.
TITLE Direct Submission
JOURNAL Submitted (08-SEP-2002) College of Veterinary Medicine, Chungbuk National University, #48, Gaehin-dong, Heungduk-ku, Cheongju 361-763, Korea

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ORIGIN

Query Match 77.3%; Score 1370.4; DB 14; Length 1768;
Best Local Similarity 89.8%; Pred. No. 0;
Matches 1533; Conservative 0; Mismatches 156; Indels 19; Gaps 5;

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RESULT 6

AP264041/c 1768 bp DNA linear VRL 23-JUL-2000
LOCUS Porcine circovirus type 2 isolate 40856 complete genome.
DEFINITION Porcine circovirus type 2 isolate 40856 complete genome.
ACCESSION AF264041
VERSION AF264041.1 GI:9392641
KEYWORDS
SOURCE Porcine circovirus 2
ORGANISM Porcine circovirus 2
VIRUSES; ssDNA viruses; Circoviridae; Circovirus.
REFERENCE 1 (bases 1 to 1768)
AUTHORS Fenaux, M., Halbur, P.G., Gill, M., Toth, T.E. and Meng, X.J.
TITLE Genetic characterization of type 2 porcine circovirus (PCV-2) from pigs with postweaning multisystemic wasting syndrome in different geographic regions of North America and development of a differential PCR-restriction fragment length with polymorphism assay to detect and differentiate between infections with PCV-1 and PCV-2
J. Clin. Microbiol. 38 (7), 2494-2503 (2000)
MEDLINE 20341537
PUBMED 10878032
REFERENCE 2 (bases 1 to 1768)
AUTHORS Fenaux, M., Halbur, P.G., Gill, M., Toth, T.E. and Meng, X.J.

TITLE Direct Submission
JOURNAL Submitted (08-MAY-2000) VMRCVM, Virginia Tech, 1410 Prices Fork Road, Blacksburg, VA 24061, USA
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ORIGIN

Query Match 77.2%; Score 1368.8; DB 14; Length 1768;
Best Local Similarity 89.7%; Pred. No. 0;
Matches 1532; Conservative 0; Mismatches 157; Indels 19; Gaps 5;
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ORIGIN	Query Match Best Local Similarity Matches 1531; Conservative	77.1%; Score 1367.2; DB 14; Length 1768; 89.6%; Pred. No. 0; 0; Mismatches 158; Indels 19; Gaps 5;	QRKDWTNVHVI VPGPCGKSKWAANFADPETTYWKPPRNKWDGTHGBBVVVDFF GWLPDDLLKRDYRLVETGKQVFPFLARSILITNSQTPLEWSSSTAIPAVALYLR RITSLVFWKNATQSTEBGQFVTLSPSPPEPEYIN"
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ACCESSION AF454546
VERSION AF454546.1 GI:18071939
KEYWORDS
SOURCE Porcine circovirus 2
ORGANISM Porcine circovirus 2
VIRUSES; ssDNA viruses; Circoviridae; Circovirus.
REFERENCE 1 (bases 1 to 1768)
AUTHORS Kim, K.M., Kim, D.Y., Park, H.S., Song, Y.K. and Kang, S.Y.
TITLE Cloning and sequencing of porcine circovirus type 2 isolated in Korea
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1768)
AUTHORS Kim, K.M., Kim, D.Y., Park, H.S., Song, Y.K. and Kang, S.Y.
TITLE Direct Submission
JOURNAL Submitted (02-DSC-2001) College of Veterinary Medicine, Chungbuk National University, 48 Gaeshin-dong, Heungduk-ku, Cheongju 361-763, Korea

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ACCESSION AF201305
VERSION AF201305.1 GI:7021343
KEYWORDS Porcine circovirus 2
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REFERENCE 1 (bases 1 to 1768)
AUTHORS Viruses; ssDNA viruses; Circoviridae; Circovirus.
Mankertz,A., Domingo,M., Folch,J.M., LeCann,P., Jestin,A.,
Segales,J., Chmielewicz,B., Plana-Duran,J. and Soike,D.
TITLE Characterisation of PCV-2 isolates from Spain, Germany and France
JOURNAL Virus Res. 66 (1), 65-77 (2000)
MEDLINE 20120936
PUBMED 10653918
REFERENCE 2 (bases 1 to 1768)
AUTHORS Mankertz,A., Domingo,M., Folch,J.M., LeCann,P., Jestin,A.,
Segales,J., Chmielewicz,B., Plana-Duran,J. and Soike,D.
TITLE Direct Submission
JOURNAL Submitted (03-NOV-1999) P24, Robert Koch Institut, Nordrufer 20,
Berlin 13353, Germany
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VERSION
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Porcine circovirus 2
Viruses: ssDNA viruses; Circoviridae; Circovirus.
1 (bases 1 to 1768)
Mankertz,A., Domingo,M., Folch,J.M., LeCann,P., Jestin,A.,
Segales,J., Chmielewicz,B., Plana-Duran,J. and Soike,D.
Characterisation of PCV-2 isolates from Spain, Germany and France
Virus Res. 66 (1), 65-77 (2000)
20120936
10653918
2 (bases 1 to 1768)
Mankertz,A., Domingo,M., Folch,J.M., LeCann,P., Jestin,A.,
Segales,J., Chmielewicz,B., Plana-Duran,J. and Soike,D.
Direct Submission
Submitted (03-NOV-1999) P24, Robert Koch Institut, Nordufer 20,
Berlin 13353, Germany
Location/Qualifiers
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ORIGIN

Query Match 75.8%; Score 1343.2; DB 14; Length 1768;

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VERSION	AF201310.1	GI:7021358	
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ORGANISM	Porcine circovirus 2		
REFERENCE	Viruses; ssDNA viruses; Circoviridae; Circovirus.		
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TITLE	Mankertz,A., Domingo,M., Folch,J.M., LeCann,P., Jestin,A.,		
JOURNAL	Segales,J., Chmielewicz,B., Plana-Duran,J. and Soike,D.		
MEDLINE	Characterisation of PCV-2 isolates from Spain, Germany and France		
PUBMED	Virus Res. 66 (1), 65-77 (2000)		
REFERENCE	20120936		
AUTHORS	10653918		
TITLE	2 (bases 1 to 1768)		
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MEDLINE	Segales,J., Chmielewicz,B., Plana-Duran,J. and Soike,D.		
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AUTHORS	Berlin 13353, Germany		
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Db	1523	TGGATACGGATCAACAGTCTCAGTAGATCATCCCAAGGTAAACAGGCATAAATCATC 1464
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Db	1463	AATAAACCACTTCTTCAACATGGTAACCATCCACACTTGTTCCTAGTGGTTTCCA 1404
Qy	303	GTAGGTGCTCCCTAGGCTCAGCAAAATTAACGGGGCCACTTGGCTCTTCCCAACCGGGCGG 362
Db	1403	GTATGTGTTTCCGGGCTGCAAAATTAGCAGCCCAATTTGCTTTTACCAACCCAGGTGG 1344
Qy	363	GCCCACTATGAGGTGATAGCTGTCTTCCATCAGCTGCTGATCTTCCGGTCACTTT 422
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Qy	483	AGTCAACCAAGAGCCCCGTCTCCAAAGGGTACTCACAGCAGTAGACAGGTGCTGCGCTT 542

Qy 1070 GGAGAGGAAATGGCATCTTCAACACCCGCTCTCCGCGACCTTCGGATATACTGTCA 1129
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